

GenCore version 5.1.6
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protein - protein search, using sw model

on: October 20, 2003, 12:23:22 ; Search time 29 Seconds

(without alignments)
606.942 Million cell updates/sec

US-09-961-201A-1

Effect score:

sequence: 1 MGFADRRLLRRLRLVEEL.....YKMPGCFNLRKLFFKTS 416

core table:

Gapop 60.0 , Gapext 60.0

searched: 328717 seqs, 42310858 residues

ord size :

total number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Listing first 75 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.p.p.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.p.p.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.p.p.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.p.p.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.p.p.*
- 6: /cgn2_6/ptodata/2/iaa/backfile1.p.p.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	416	100.0	416	3	US-08-852-936C-1
2	416	100.0	416	3	US-09-300-328-1
3	416	100.0	416	4	US-09-069-023-23
4	219	52.6	416	4	US-09-561-756-30
5	219	52.6	416	4	US-09-227-721-30
6	202	48.6	203	3	US-08-852-936C-4
7	202	48.6	203	3	US-09-300-328-4
8	195	46.9	416	3	US-09-257-218-2
9	195	46.9	416	3	US-09-311-760-2
10	195	46.9	416	4	US-08-865-579-2
11	195	46.9	416	4	US-10-059-749-2
12	15	3.6	15	3	US-09-257-218-22
13	15	3.6	15	3	US-09-311-760-22
14	15	3.6	15	4	US-09-561-756-59
15	15	3.6	15	4	US-09-227-721-59
16	15	3.6	15	4	US-08-865-579-22
17	15	3.6	15	4	US-10-059-749-22
18	15	3.6	46	3	US-09-257-218-6
19	15	3.6	46	3	US-09-311-760-6
20	15	3.6	46	4	US-08-865-579-6
21	15	3.6	46	4	US-10-059-749-6
22	11	2.6	299	2	US-08-773-608A-2
23	10	2.4	39	4	US-09-187-789-38
24	10	2.4	39	4	US-09-139-600-33
25	10	2.4	303	3	US-08-462-969B-2
26	10	2.4	303	4	US-09-561-756-24
27	10	2.4	303	4	US-09-227-721-24

28	10	2.4	303	4	US-08-556-627A-2	Sequence 2, Appli
29	10	2.4	303	4	US-09-124-934A-2	Sequence 2, Appli
30	10	2.4	303	4	US-08-724-378D-4	Sequence 4, Appli
31	10	2.4	303	4	US-08-334-251D-2	Sequence 2, Appli
32	10	2.4	346	2	US-08-618-408B-2	Sequence 2, Appli
33	10	2.4	389	4	US-08-724-378D-2	Sequence 2, Appli
34	10	2.4	389	4	US-08-724-378D-3	Sequence 3, Appli
35	10	2.4	479	1	US-08-665-220-2	Sequence 2, Appli
36	10	2.4	479	3	US-09-291-692-2	Sequence 2, Appli
37	10	2.4	479	4	US-09-561-756-33	Sequence 33, Appli
38	10	2.4	479	4	US-09-227-721-33	Sequence 33, Appli
39	10	2.4	521	4	US-09-962-834A-2	Sequence 2, Appli
40	9	2.2	9	3	US-09-257-218-19	Sequence 19, Appli
41	9	2.2	9	3	US-09-311-760-19	Sequence 19, Appli
42	9	2.2	9	4	US-09-561-756-56	Sequence 56, Appli
43	9	2.2	9	4	US-09-227-721-56	Sequence 56, Appli
44	9	2.2	9	4	US-08-865-579-19	Sequence 19, Appli
45	9	2.2	9	4	US-10-059-749-19	Sequence 19, Appli
46	9	2.2	1196	3	US-08-881-706-2	Sequence 2, Appli
47	8	1.9	141	4	US-09-252-991A-16951	Sequence 16951, A
48	8	1.9	1218	4	US-09-198-452A-98	Sequence 98, Appli
49	7	1.7	25	4	US-09-257-179-96	Sequence 96, Appli
50	7	1.7	141	4	US-09-252-991A-25224	Sequence 25224, A
51	7	1.7	150	4	US-09-198-452A-1023	Sequence 1023, AP
52	7	1.7	202	4	US-09-257-179-90	Sequence 90, Appli
53	7	1.7	248	4	US-09-252-991A-29249	Sequence 29249, A
54	7	1.7	253	4	US-09-252-991A-22878	Sequence 22878, A
55	7	1.7	304	4	US-09-252-991A-23222	Sequence 23222, A
56	7	1.7	313	4	US-09-252-991A-30181	Sequence 30181, A
57	7	1.7	318	4	US-09-292-858B-24	Sequence 24, Appli
58	7	1.7	324	4	US-09-328-352-6612	Sequence 6612, Ap
59	7	1.7	339	4	US-09-252-991A-27713	Sequence 27713, A
60	7	1.7	369	4	US-09-252-991A-23356	Sequence 23356, A
61	7	1.7	401	1	US-08-198-446B-11	Sequence 11, Appli
62	7	1.7	419	2	US-08-870-693-11	Sequence 11, Appli
63	7	1.7	419	4	US-09-134-001C-3441	Sequence 3441, Ap
64	7	1.7	423	4	US-09-328-352-6273	Sequence 6273, Ap
65	7	1.7	426	4	US-09-252-991A-29288	Sequence 29288, A
66	7	1.7	434	4	US-09-252-991A-27235	Sequence 27235, A
67	7	1.7	448	2	US-08-878-989-2	Sequence 2, Appli
68	7	1.7	448	3	US-09-272-796-2	Sequence 2, Appli
69	7	1.7	508	3	US-09-344-700-4	Sequence 25, Appli
70	7	1.7	550	1	US-08-143-219-25	Sequence 9, Appli
71	7	1.7	551	2	US-08-436-771-9	Sequence 9, Appli
72	7	1.7	551	2	US-08-434-998-9	Sequence 9, Appli
73	7	1.7	551	5	PCT-US95-02058-9	Sequence 9, Appli
74	7	1.7	551	5	PCT-US95-02058-9	Sequence 3, Appli
75	7	1.7	733	3	US-09-073-587-3	

A IGNMENTS

RESULT 1

US-08-852-936C-1

; Sequence 1, Application US/08852936C

; Patent No. 6010878

; GENERAL INFORMATION:

; APPLICANT: DIXIT, VISHVA M.

; APPLICANT: HE, WEI-WU

; APPLICANT: KIKLY, KRISTINE K.

; APPLICANT: RUBEN, STEVEN M.

; TITLE OF INVENTION: INTERLEUKIN 1 BETA CONVERTING

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,936C
FILING DATE: 08-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-936C-1

Query Match 100.0%; Score 416; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRLRLVEELQVQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
DB 1 MDEADRLRLRLRLVEELQVQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGHCLIIINNVPFCRESGLRTR 180
DB 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRRFRSSLHFVVEKGLDTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
DB 181 TGSNIDCEKLRRRFRSSLHFVVEKGLDTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
QY 241 ASHLQFPAGVYGTDCGCVSVSEKIVNIFNGTSCPSLGKPKLFFIACCGEQKHGFEVAS 300
DB 241 ASHLQFPAGVYGTDCGCVSVSEKIVNIFNGTSCPSLGKPKLFFIACCGEQKHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISLPTPSDIFVSYSTFCFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISLPTPSDIFVSYSTFCFVSWRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDQSLRLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
DB 361 SWYVETLDDIFQWAHSEDQSLRLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 2

US-09-300-328-1
Sequence 1, Application US/09300328
Patent No. 6294169
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: HE, WEI-WU
APPLICANT: KIRLY, KRISTINE K.

APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,328
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,936
FILING DATE: 08-MAY-1997
APPLICATION NUMBER: 0/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
us-09-300-328-1
Query Match 100.0%; Score 416; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDEADRLRLRLRLVEELQVQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
DB 1 MDEADRLRLRLRLVEELQVQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNRQAGKSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGHCLIIINNVPFCRESGLRTR 180
DB 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRRFRSSLHFVVEKGLDTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
DB 181 TGSNIDCEKLRRRFRSSLHFVVEKGLDTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
QY 241 ASHLQFPAGVYGTDCGCVSVSEKIVNIFNGTSCPSLGKPKLFFIACCGEQKHGFEVAS 300
DB 241 ASHLQFPAGVYGTDCGCVSVSEKIVNIFNGTSCPSLGKPKLFFIACCGEQKHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISLPTPSDIFVSYSTFCFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISLPTPSDIFVSYSTFCFVSWRDPKSG 360

GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: HE, WEI-WU
APPLICANT: KIKLY, KRISTINE K.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852.936C
FILING DATE: 08-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-936C-4

Query Match 48.6%; Score 202; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.2e-186;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 212 MVLALLELARQDHGALDCCVVVILSHGCCQASHLQFPAGVYGTGDCPVSVEKIVNIFNGTS 271
Db 1 MVLALLELARQDHGALDCCVVVILSHGCCQASHLQFPAGVYGTGDCPVSVEKIVNIFNGTS 60
Qy 272 CPSLGGKPKLFFIOACCGEQKHGFVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDA 331
Db 61 CPSLGGKPKLFFIOACCGEQKHGFVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDA 120
Qy 332 ISSLPTSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAV 391
Db 121 ISSLPTSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAV 180
Qy 392 SVKGIYKQMPGCFNFKLFF 413
Db 181 SVKGIYKQMPGCFNFKLFF 202

RESULT 7
US-09-300-328-4
; Sequence 4, Application US/09300328
; Patent No. 6294169

GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: HE, WEI-WU
APPLICANT: KIKLY, KRISTINE K.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,328
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,936
FILING DATE: 08-MAY-1997
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-328-4

Query Match 48.6%; Score 202; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.2e-186;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 212 MVLALLELARQDHGALDCCVVVILSHGCCQASHLQFPAGVYGTGDCPVSVEKIVNIFNGTS 271
Db 1 MVLALLELARQDHGALDCCVVVILSHGCCQASHLQFPAGVYGTGDCPVSVEKIVNIFNGTS 60
Qy 272 CPSLGGKPKLFFIOACCGEQKHGFVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDA 331
Db 61 CPSLGGKPKLFFIOACCGEQKHGFVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDA 120
Qy 332 ISSLPTSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAV 391
Db 121 ISSLPTSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAV 180
Qy 392 SVKGIYKQMPGCFNFKLFF 413
Db 181 SVKGIYKQMPGCFNFKLFF 202

RESULT 8
US-09-257-218-2

Sequence 2, Application US/09257218
Patent No. 6271361

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa

APPLICANT: Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

TITLE OF INVENTION: Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/257,218

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/865,579

FILING DATE: 29-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 416 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-257-218-2

Query Match

Best Local Similarity 46.9%; Score 195; DB : Length 416;

Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

222 QDHGALDCCVWVILSHGCOASHLOFPFVAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

222 QDHGALDCCVWVILSHGCOASHLOFPFVAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

282 FFIQACGGEQKHGFVASTSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTSPSDI 341

282 FFIQACGGEQKHGFVASTSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTSPSDI 341

342 FVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMP 401

342 FVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMP 401

402 GCFNFKLKKLFFKTS 416

402 GCFNFKLKKLFFKTS 416

RESULT 9

US-09-311-760-2

Sequence 2, Application US/09311760

Patent No. 6274318

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa

APPLICANT: Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/311,760

FILING DATE: 13-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/865,579

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 416 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-311-760-2

Query Match

Best Local Similarity 46.9%; Score 195; DB 3; Length 416;

Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

222 QDHGALDCCVWVILSHGCOASHLOFPFVAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

222 QDHGALDCCVWVILSHGCOASHLOFPFVAVGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

282 FFIQACGGEQKHGFVASTSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTSPSDI 341

282 FFIQACGGEQKHGFVASTSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTSPSDI 341

342 FVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMP 401

342 FVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMP 401

402 GCFNFKLKKLFFKTS 416

402 GCFNFKLKKLFFKTS 416

RESULT 10

US-08-865-579-2

Sequence 2, Application US/08865579

Patent No. 6453296

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa

APPLICANT: Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

TITLE OF INVENTION: Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9849
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-865-579-2

Query Match 46.9%; Score 195; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.3e-179;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 222 QDHGALDCCVVVILSHGCOASHLQFGAVYGTGCPVSVVEKIWNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVVILSHGCOASHLQFGAVYGTGCPVSVVEKIWNIFNGTSCPSLGGKPKL 281
Qy 282 FFIQACGGEOKDHGFVASTSPEDSPGNSNPEDATPFOEGLRTFDQDLDAISLTPSDI 341
Db 282 FFIQACGGEOKDHGFVASTSPEDSPGNSNPEDATPFOEGLRTFDQDLDAISLTPSDI 341
Qy 342 FVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKMP 401
Db 342 FVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKMP 401
Qy 402 GCFNFLRKKLFFKTS 416
Db 402 GCFNFLRKKLFFKTS 416

RESULT 11
US-10-059-749-2
Sequence 2, Application US/10059749
Patent No. 6566505
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
ENCODING SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749

FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match 46.9%; Score 195; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.3e-179;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 222 QDHGALDCCVVVILSHGCOASHLQFGAVYGTGCPVSVVEKIWNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVVILSHGCOASHLQFGAVYGTGCPVSVVEKIWNIFNGTSCPSLGGKPKL 281
Qy 282 FFIQACGGEOKDHGFVASTSPEDSPGNSNPEDATPFOEGLRTFDQDLDAISLTPSDI 341
Db 282 FFIQACGGEOKDHGFVASTSPEDSPGNSNPEDATPFOEGLRTFDQDLDAISLTPSDI 341
Qy 342 FVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKMP 401
Db 342 FVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKMP 401
Qy 402 GCFNFLRKKLFFKTS 416
Db 402 GCFNFLRKKLFFKTS 416

RESULT 12
US-09-257-218-22
Sequence 22, Application US/09257218
Patent No. 6271361
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
ENCODING SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,218
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
S-09-257-218-22

Query Match 3.6%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 350 GFVSWRDPKSGSWYV 364
| | | | | | | | | | | | | | | |
Db 1 GFVSWRDPKSGSWYV 15

RESULT 13
IS-09-311-760-22
Sequence 22, Application US/09111760
Patent No. 6274118
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
 Fernandes-Alnemri, Teresa
 Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/311,760
FILING DATE: 13-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/865,579
APPLICATION DATE:
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-311-760-22

Query Match 3.6%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 350 GFVSWRDPKSGSWYV 364
| | | | | | | | | | | | | | | |
Db 1 GFVSWRDPKSGSWYV 15

RESULT 14
US-09-561-756-59
Sequence 59, Application US/09561756
Patent No. 6376226
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapien
US-09-561-756-59

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 350 GFVSWRDPKSGSWYV 364
| | | | | | | | | | | | | | | |
Db 1 GFVSWRDPKSGSWYV 15

RESULT 15
US-09-227-721-59
Sequence 59, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-59

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 350 GFVSWRDPKSGSWYV 364
| | | | | | | | | | | | | | | |
Db 1 GFVSWRDPKSGSWYV 15

RESULT 16
US-08-865-579-22
Sequence 22, Application US/08865579
Patent No. 6455296
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
 Fernandes-Alnemri, Teresa
 Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 Encoding Same and Methods of Use
US-08-865-579-22

NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-865-579-22

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 17
US-10-059-749-22
Sequence 22, Application US/10059749
Patent No. 6566505
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
FERNANDES-ALNEMRI, TERESA
LITWACK, GERALD
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-059-749-22

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 18
US-09-257-218-6
Sequence 6, Application US/09257218
Patent No. 6271361
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
FERNANDES-ALNEMRI, TERESA
LITWACK, GERALD
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,218
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-257-218-6

Query Match 3.6%; Score 15; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364

b 32 GFVSWRDPKSGSWYV 46
|||||

ESULT 19

S-09-311-760-6

Sequence 6, Application US/09311760

Patent No. 6274318

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

Fernandes-Alnemri, Teresa

Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/311,760

FILING DATE: 13-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/865,579

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 46 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-311-760-6

Query Match

Best Local Similarity 3.6%; Score 15; DB 3; Length 46;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364

Db 32 GFVSWRDPKSGSWYV 46

RESULT 20

US-08-865-579-6

Sequence 6, Application US/08865579

Patent No. 6455296

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa

APPLICANT: Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-865-579-6

Query Match 3.6%; Score 15; DB 4; Length 46;

Best Local Similarity 100.0%; Pred. No. 4.8e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364

Db 32 GFVSWRDPKSGSWYV 46

RESULT 21

US-10-059-749-6

Sequence 6, Application US/10059749

Patent No. 6566505

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

Fernandes-Alnemri, Teresa

Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/059,749

FILING DATE: 29-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/865,579

FILING DATE: 29-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-059-749-6

Query Match 3.6%; Score 15; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
|||'|||||
DB 32 GFVSWRDPKSGRWYV 46

RESULT 22
US-08-773-608A-2
; Sequence 2, Application US/08773608A
; Patent No. 5858778
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Sf Caspase-i, Compositions and Methods
; TITLE OF INVENTION: for Making and Methods of Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5858778ris
; STREET: One Liberty Place 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19355
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,608A
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-773-608A-2

Query Match 2.6%; Score 11; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
|||'|||||
DB 168 GKPKLFFIQAC 178

RESULT 23
US-09-187-789-38
; Sequence 38, Application US/09187789

Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140-434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-38

Query Match 2.4%; Score 10; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287
|||'|||||
DB 21 KPCLFFIQAC 30

RESULT 24
US-09-139-600-33
; Sequence 33, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140-434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-33

Query Match 2.4%; Score 10; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287
|||'|||||
DB 21 KPCLFFIQAC 30

RESULT 25
US-08-462-969B-2
; Sequence 2, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/462,969B
FILING DATE: 05-JUN-1995
CLASSIFICATION: S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF140P1
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-462-969B-2

Query Match 2.4%; Score 10; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

iy 278 KPCLFFIQAC 287
|||||
b 177 KPCLFFIQAC 186

RESULT 26
US-09-561-756-24
Sequence 24, Application US/09561756
Patent No. 6376226
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapien
US-09-561-756-24

Query Match 2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFIQAC 287
|||||
Db 177 KPCLFFIQAC 186

RESULT 27
US-09-227-721-24
Sequence 24, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-24

FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE: 05-JUN-1995
CLASSIFICATION: S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF140P1
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-462-969B-2

Query Match 2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFIQAC 287
|||||
Db 177 KPCLFFIQAC 186

RESULT 28
US-08-556-627A-2
Sequence 2, Application US/08556627A
Patent No. 6462175
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Eresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch1, A No. 6462175el Apoptotic Protease,
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,627A
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-556-627A-2

Query Match 2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFIQAC 287
|||||
Db 177 KPCLFFIQAC 186

RESULT 29

S-09-124-934A-2

Sequence 2, Application US/09124934A

Patent No. 6495519

GENERAL INFORMATION:

APPLICANT: He Wei-Wu et al.

TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 an

FILE REFERENCE: PF140C1

CURRENT APPLICATION NUMBER: US/09/124,934A

CURRENT FILING DATE: 1994-11-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 303

TYPE: PR1

ORGANISM: homo sapiens

S-09-124-934A-2

Query Match 2.4%; Score 10; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 278 KPKLFFFIQAC 287

Db 177 KPKLFFFIQAC 186

|||||

RESULT 30

JS-08-724-378D-4

Sequence 4, Application US/08724378D

Patent No. 6512104

GENERAL INFORMATION:

APPLICANT: JUAN, SHAO-CHIEH

APPLICANT: FLETCHER, FREDERICK A.

APPLICANT: PATTERSON, SCOTT D.

TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE

TITLE OF INVENTION: PROTEASE

FILE REFERENCE: 06843-0019-00000

CURRENT APPLICATION NUMBER: US/08/724,378D

CURRENT FILING DATE: 1996-10-01

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 303

TYPE: PR1

ORGANISM: Homo sapiens

US-08-724-378D-4

Query Match 2.4%; Score 10; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287

Db 177 KPKLFFFIQAC 186

|||||

RESULT 31

US-08-334-251D-2

Sequence 2, Application US/08334251D

Patent No. 6538121

GENERAL INFORMATION:

APPLICANT: He et al.

TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 an

FILE REFERENCE: PF140

CURRENT APPLICATION NUMBER: US/08/334,251D

CURRENT FILING DATE: 1994-11-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 303

TYPE: PR1

ORGANISM: Homo sapiens

US-08-334-251D-2

Query Match 2.4%; Score 10; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287

Db 177 KPKLFFFIQAC 186

|||||

RESULT 32

US-08-618-408B-2

Sequence 2, Application US/08618408B

Patent No. 5851815

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa

APPLICANT: Litwack, Gerald

APPLICANT: Armstrong, Robert

APPLICANT: Tomaselli, Kevin

TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic

TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/618,408B

FILING DATE: 19-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 1957

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 346 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-618-408B-2

Query Match 2.4%; Score 10; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287

Db 216 KPKLFFFIQAC 225

|||||

RESULT 33

US-08-724-378D-2

Sequence 2, Application US/08724378D

Patent No. 6512104

GENERAL INFORMATION:

APPLICANT: JUAN, SHAO-CHIEH

APPLICANT: FLETCHER, FREDERICK A.

APPLICANT: PATTERSON, SCOTT D.

TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE

TITLE OF INVENTION: PROTEASE
FILE REFERENCE: 06843-0019-00000
CURRENT APPLICATION NUMBER: US/08/724,378D
CURRENT FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 389
TYPE: PRT
ORGANISM: Homo sapiens
S-08-724-378D-2

Query Match 2.4%; Score 10; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 278 KPKLFFFIQAC 287
|||||
b 259 KPKLFFFIQAC 268
|||||

RESULT 34
IS-08-724-378D-3
Sequence 3, Application US/08724378D
Patent No. 6512104
GENERAL INFORMATION:
APPLICANT: JUAN, SHAO-CHIEH
APPLICANT: FLETCHER, FREDERICK A.
APPLICANT: PATTERSON, SCOTT D.
TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
FILE REFERENCE: 06843-0019-00000
CURRENT APPLICATION NUMBER: US/08/724,378D
CURRENT FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 389
TYPE: PRT
ORGANISM: Homo sapiens
US-08-724-378D-3

Query Match 2.4%; Score 10; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287
|||||
Db 259 KPKLFFFIQAC 268
|||||

RESULT 35
US-08-665-220-2
Sequence 2, Application US/08665220
Patent No. 5786173
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,220
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/618,408
FILING DATE: 19-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-220-2

Query Match 2.4%; Score 10; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287
|||||
Db 349 KPKLFFFIQAC 358
|||||

RESULT 36
US-09-291-692-2
Sequence 2, Application US/09291692
Patent No. 6287795
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,692
FILING DATE: 04-13-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 480140.424C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-09-291-692-2

Query Match 2.4%, Score 10; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFFIQAC 287
|
Db 349 KPCLFFFIQAC 358
|

RESULT 37

US-09-561-756-33
; Sequence 33, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-33

Query Match 2.4%, Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFFIQAC 287
|
Db 349 KPCLFFFIQAC 358
|

RESULT 38

US-09-227-721-33
; Sequence 33, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227.721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-33

Query Match 2.4%, Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFFIQAC 287
|
Db 349 KPCLFFFIQAC 358
|

RESULT 39

US-09-962-834A-2
; Sequence 2, Application US/09962834A
; Patent No. 6586225
; GENERAL INFORMATION:

APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.3, Version #1.30
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,834A
FILING DATE: 25-Sep-2001
CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,123
FILING DATE: 1996-07-03
; ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2

Query Match 2.4%, Score 10; DB 4; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFFIQAC 287
|
Db 392 KPCLFFFIQAC 401
|

RESULT 40

US-09-257-218-19
; Sequence 19, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,218
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579

FILING DATE: 29-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

S-09-257-218-19

Query Match 2.2%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Y 283 FIOACGGEQ 291
Db 1 FIOACGGEQ 9

RESULT 41

US-09-311-760-19

Sequence 19, Application US/09311760

Patent No. 6274318

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

Fernandes-Alnemri, Teresa

Litwack, Gerald

TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

Encoding Same and Methods of Use

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 87

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/311,760

FILING DATE: 13-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/865,579

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-311-760-19

Query Match 2.2%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 283 FIOACGGEQ 291
Db 1 FIOACGGEQ 9

RESULT 42

US-09-561-756-56

Sequence 56, Application US/09561756

Patent No. 6376226

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

FILE OF INVENTION: THEREOF

FILE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/561,756

CURRENT FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: 09/227,721

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 56

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapien

US-09-561-756-56

Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 283 FIOACGGEQ 291
Db 1 FIOACGGEQ 9

RESULT 43

US-09-227-721-56

Sequence 56, Application US/09227721

Patent No. 6379950

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

FILE OF INVENTION: THEREOF

FILE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/227,721

CURRENT FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 56

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapien

US-09-227-721-56

Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 283 FIOACGGEQ 291
Db 1 FIOACGGEQ 9

RESULT 44

US-08-865-579-19
Sequence 19, Application US/08865579
Patent No. 6455296
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
TITLE OF INVENTION: Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-865-579-19

Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 FIOACGGEQ 291
|||
Db 1 FIOACGGEQ 9

RESULT 45

US-10-059-749-19
Sequence 19, Application US/10059749
Patent No. 6566505
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
TITLE OF INVENTION: Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-059-749-19

Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 FIOACGGEQ 291
|||
Db 1 FIOACGGEQ 9

RESULT 46

US-08-881-706-2
Sequence 2, Application US/08881706
Patent No. 6245969
GENERAL INFORMATION:
APPLICANT: Chong, Joane
APPLICANT: Li, Jianming
TITLE OF INVENTION: Receptor Kinase BIN1
FILE REFERENCE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/881,706
CURRENT FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1196
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-08-881-706-2

Query Match 2.2%; Score 9; DB 3; Length 1196;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 IGSFGFGDV 139
|||
Db 889 IGSFGFGDV 897

RESULT 47

US-09-252-991A-16951
Sequence 16951, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

```
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16951
LENGTH: 141
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16951

Query Match      1.9%; Score 8; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 45 RAGSGSRR 52
| | | | |
b 114 RAGSGSRR 12;

RESULT 48
US-09-198-452A-98
Sequence 98, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffaia, R
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 98
LENGTH: 1218
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: SITE
LOCATION: 1...1218
OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-98

Query Match      1.9%; Score 8; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 377 SEDLOSLL 384
| | | | |
b 198 SEDLOSLL 205

RESULT 49
US-09-257-179-96
Sequence 96, Application US/09257179
Patent No. 6410709
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 96
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-257-179-96

Query Match      1.7%; Score 7; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 223 DHGALDC 229
| | | | |
b 13 DHGALDC 19

RESULT 50
US-09-252-991A-25224
Sequence 25224, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25224
LENGTH: 141
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25224

Query Match      1.7%; Score 7; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 140 GALESLR 146
| | | | |
b 124 GALESLR 130

Search completed: October 20, 2003, 12:28:30
Job time : 32 secs
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Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
Accession: JC7123
Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
J. Biochem. Biophys. Res. Commun. 264, 550-555, 1999
Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
Reference number: JC7123; MUID:20001956; PMID:10529400
Accession: JC7123
Status: preliminary
Molecule type: mRNA
Residues: 1-454 <FUJ>
Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 76.1%; Score 1658; DB 2; Length 454;
Best Local Similarity 72.5%; Pred. No. 4.8e-134;
Matches 329; Conservative 24; Mismatches 63; Indels 38; Gaps 2;

1 MDEADRLRLRCLRLVEELQVQDLNDVLSREL FMTEDIORAGSGRRDQARQLII 60
1 MDEADRLRLRCLRLVLSLQVLAELWALSLRSLFTRDIEDTCQAGSGRRDQARQLVT 60
61 DLETRGQALPLFTISCLEDTCQDMLASFLRTNRQAGL----- 98
61 DLETRGQALPLFTISCLEDTCQDMLASFLRTNRQAGL----- 98
99 -----SKPTLENLTPVVLRLP----- <PEVLRLP>PRPVDIGSGGFGDVGAL 142
121 AKGQVVLKLEPSQPAVGNLTPVVLGPEELWP; <PEVLRLP>PRPVDIGSGGFGDVGCP 180
143 ESLRGNADLAYILSMPCGCHLIINNVPFCREGLTRTGSNIDCEKLRFRSSLFHFMVE 202
181 GKIRGNADLAYILSMPCGCHLIINNVPFCREGLTRTGSNIDCEKLRFRRLREWVE 240
203 VKGDLTAKMVALLELRLQDHCALDCCVVVILSHGQASHLOFPQAVYGTGDCPVSVSEK 262
241 VKNDLTAKMVALLELRLQDHCALDCCVVVILSHGQASHLOFPQAVYGTGDCPVSVSEK 300
263 IVNIFNGTSCPSLGGKPKLFFIOACGGEQKHGFVEASTSPEDSPGNSPEPDATPFQEG 322
301 IVNIFNGTSCPSLGGKPKLFFIOACGGEQKHGFVEASTSPEDSPGNSPEPDATPFQEG 360
323 LRTFQQLDALSSTLPTSDIFVSSTPGFVSWRDPKSGSWYVETLDDIFEQWASEDLQS 382
361 PRPQQLDALSSTLPTSDIFVSSTPGFVSWRDPKSGSWYVETLDDIFEQWASEDLQS 420
383 LLLRVANAVSKGIYKMPGCFNFKLKKFFKTS 416
421 LLLRVANAVSKGIYKMPGCFNFKLKKFFKTS 454

RESULT 3
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
Accession: S64710; S72395
R:Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
A:Reference number: S64710; MUID:96183185; PMID:8605870
A:Accession: S64710
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-277 <WAN>
A:Cross-references: EMBL:U27463
R:Wang, X.
submitted to the EMBL Data Library, May 1995
A:Reference number: S72395
A:Accession: S72395
A:Molecule type: mRNA
A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <WAN>
A:Cross-references: EMBL:U27463; NID:91244443; PID:91244444
C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.7%; Score 429; DB 2; Length 277;
Best Local Similarity 33.2%; Pred. No. 5e-29;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

150 DLAYILSMPCGCHLIINNVPFCREGLTRTGSNIDCEKLRFRSSLFHFMVEVKGLDITA 209
34 DSSYKMDYPDMGVCIIINNKNFKSTGMTPRSGTDVDAAKLRETFMNLKYEVNRKNDLTR 93
210 KMWLALLELRLQDHCALDCCVVVILSHGQASHLOFPQAVYGTGDCPVSVSEKIVNIFNG 269
94 EEIVELMRVSKDEHSHKSSSFVCVLSHGDE-----GVIFGTG-PIDUKLTSTFPG 145
270 TSCPSLGGKPKLFFIOACGGEQKHGFVEASTSPEDSPGNSPEPDATPFQEGRLTFDQL 329
146 DRCRLSLGPKLFIIOACRGTELDGCIETDSGTEDMT----- 183
330 DAISLPTSDIFVSSTPGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVAN 389
184 --COKIPVEADFLYASTAGYYSWRNPKDGSWFQSLCSMLKLYAHKLEPMHILTRNR 241
390 AVSVK-----GIYKMPGCFNFKLKKFF 413
242 KVATEPESFSLDSTFHAKQIPICVISMLTKELYP 275

RESULT 4
A55315
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
N:Alternate names: cysteine proteinase CPP32
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
Accession: A55315; S58899; I39005
R:Bernandee-Alnemri, I.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
A:Reference number: A55315; MUID:95074098; PMID:7983002
A:Accession: A55315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <FER>
A:Cross-references: GB:U13737; NID:9561665; PID:AAA65015.1; PID:9561666
R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,
Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalia
A:Reference number: S58899; MUID:95319529; PMID:7596430
A:Accession: S58899
A:Molecule type: protein
A:Residues: 29-46; 176-189, 'E', 191-193 <NIC>
R:Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier
Cell 81, 801-809, 1995
Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A:Reference number: A56924; MUID:95292347; PMID:7774019
A:Accession: I39005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-189, 'E', 191-277 <RES>
A:Cross-references: EMBL:U26943; NID:9857568; PID:AAA74929.1; PID:9857569
C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 19.2%; Score 418; DB 2; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.4e-28;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

150 DLAYILSMPCGCHLIINNVPFCREGLTRTGSNIDCEKLRFRSSLFHFMVEVKGLDITA 209
34 DSSYKMDYPDMGVCIIINNKNFKSTGMTPRSGTDVDAAKLRETFMNLKYEVNRKNDLTR 93
210 KMWLALLELRLQDHCALDCCVVVILSHGQASHLOFPQAVYGTGDCPVSVSEKIVNIFNG 269
94 EEIVELMRVSKDEHSHKSSSFVCVLSHGDE-----GVIFGTG-PVDUKLTSTFPG 145
270 TSCPSLGGKPKLFFIOACGGEQKHGFVEASTSPEDSPGNSPEPDATPFQEGRLTFDQL 329

b 146 DRCSRLTGKPKLPIIOACRGTELDGCIETDSGVDDDM----- 182
 330 DAISLPTSDIDFVSVSTPFGVSWRDPKSGSWYVETLDDIFEQWASHEDLSQSLLRVAN 389
 183 -ACHKIPVDADFLYAVSTAGYYSWNSKGSNFWTOSLCMLKQYADKLEFPHILTRVNR 241
 390 AVSVK-----GIYQMPCCFNLKRLUFF 413
 242 KVATEFESFDFATFAKQIPICVSMILTKELYF 275

ESULT 5
 C6507
 apase-2 - rat
 ;Species: Rattus norvegicus (Norway rat)
 ;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 ;Accession: JC6507
 ;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 ;Title: Cloning and expression of the cDNA encoding rat caspase-2.
 ;Reference number: JC6507; MUID:98087427; PMID:9427555
 ;Accession: JC6507
 ;Status: preliminary
 ;Molecule type: mRNA
 ;Residues: 1-452 <SAT>
 ;Cross-references: GB:U77933; NID:92769705; PIDN:AB96379.1; PID:92769706

Query Match 19.0%; Score 414; DB 2; Length 452;
 Best Local Similarity 28.5%; Pred. No. 1.9e-27;
 Matches 125; Conservative 65; Mismatches 154; Indels 94; Gaps 12;

2Y 4 ADRR-----LLRCLRLVVEELQQLMDVLLSRLFRPHMLEDIQRAGS 48
 20 ADRSRILAVCGHDPHQETLKKNRVVLAKQLLSLEHLEKDIITLEMRELIIQ--AK 77
 2Y 49 GRRDQARQLIIDLETRGSQALPLFISCLEDTJOMLASFLRTN----- 92
 78 GGSFQNVLLNLLPKRGQAFDAFCEALRETGHLEDLTLTLSDIQTLPPLSCDYD 137
 2Y 93 -----RQAGLSKPTLENLT-----PVLRPEIRKPEVLRPPTPRVDIGSG 134
 138 SSLPFSVCSCPHKOSRLSTDTMHSUNGDPGVCLO-----VKPCTP----- 181
 2Y 135 GFGDVGALSLRGNADLAYILSMFCGCHGLIINNFCRESGLRTRTGSNIDCEKLRFRF 194
 182 -----EFYQAHYQLAYRLOSQPRGLALVMSNHFTEKDLFRSGDVHDTTLTLF 233
 2Y 195 SSLHFWVEYKGLTAKKVVALLLELAR-ODHGALDCCVVVILSHGCGQASHLOFPGAVYGT 253
 234 KLLGYNVHLYDQTAQAEQKLEONFAQLPAHRVTDSCIVALLSHGVE-----GGIYGV 286
 2Y 254 DGCPSVSEKIVNIFNGTSCPSLGGKPKLFFFIQACGEGKDHGFEVASTSPEDSPGNSPE 313
 287 DCKLLQLOEVFLFNANCPSLONPKPFFFIQACRGDETRGVQDQKKNHAGSPGCE-E 345
 2Y 314 PRATPFOGLRTFDOLDLAISSLPTSDIFVSVSTPFGVSWRDPKSGSWYVETLDDIFEQ 373
 346 SDAG--KEELMKM-----RLPTRSDMICGYACKGNAAAMRNTKRGSWYIEALTQVFE 396
 374 WAHSEDLQSLLRVANAV 391
 397 RACDMHVADMLVKV-NAL 413

RESULT 6
 A54821
 apoptotic regulator ICH-1, stimulatory form L - human
 ;Species: Homo sapiens (man)
 ;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 ;Accession: A54821
 ;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994

A;Title: ICH-1, an Ice/ced-3-related gene, encodes both positive and negative regulator
 A;Reference number: A54821; MUID:94373811; PMID:8087842
 A;Accession: A54821
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-435 <WAN>
 A;Cross-references: GB:U13021; NID:9537291; PID:9537292
 C;Keywords: alternative splicing; apoptosis

Query Match 18.8%; Score 409; DB 2; Length 435;
 Best Local Similarity 29.5%; Pred. No. 4.8e-27;
 Matches 127; Conservative 66; Mismatches 155; Indels 82; Gaps 13;

QY 9 LRRCLRLVEELQVQDQMDVLLSRLFRPHMLEDIQ-RAGSGSRDDQARQLIIDLETRGS 67
 DB 23 LKKNRVVLAKQLLSLEHLEKDIITLEMRELIIQKVGSPS---QNVLLNLLPKRGP 79
 QY 68 QALPLFISCLEDTGQDMLASFLRTN-----RQAGKL 98
 DB 80 QAFDAFCEALRETQGHLEDMILLTTLGLQHLVPLPSCDYDLSLPPVCESCPLYKKLRL 139
 QY 99 SKPTLENLT-----PVLRPEIRKPEVLRPPTPRVDIGSGGFGDVGALSLRGNADLAY 153
 DB 140 STDTVEHSLDNKDGVCLO-----VKPCTP-----EFYQTHFQLAY 175
 QY 154 ILSMEFCGCHGLIINNFCRESGLRTRTGSNIDCEKLRFRFSSLHFMVEYKGLTAKKVV 213
 DB 176 RLOSRRGLALVLSNVHFTGKELEFRSGDVHDTLTLFKLLGYDVHVLCDQTAQEMQ 235
 QY 214 LALLELAR-QDHGALDCCVVVILSHGCGQASHLOFPGAVYGTGCPVSEKIVNIFNGTSC 272
 DB 236 EKLNFAQLPAHRVTDSCIVALLSHGVE-----GAIYGVDCKLLQLOEVFQLEFNANC 288
 QY 273 PSLGGKPKLFFFIQACGEGKDHGFEVASTSPEDSPGNSPEPDATPFOGLRTFDQDAI 332
 DB 289 PSLQNKPKMFFFIQACRGDETRGVQDQKKNHAGSPGCE-ESDA-----GKEKLPKM--- 339
 QY 333 SSILPTSDIFVSVSTPFGVSWRDPKSGSWYVETLDDIFEQWASHEDLSQSLLRVANAVS 392
 DB 340 -RLPTRSDMICGYACLKGTAAAMRNTKRGSWYIEALQVSEACDMHVADMLVKV-NAL- 396
 QY 393 VKGIYKQMPG 402
 DB 397 IKDREGYAPG 406

RESULT 7
 JC5410
 Cpp32 protein - mouse
 ;Species: Mus musculus (house mouse)
 ;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 ;Accession: JC5410
 ;Mukasa, T.; Urabe, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 ;Biochem. Biophys. Res. Commun. 231, 770-774, 1997
 A;Title: Specific expression of Cpp32 in sensory neurons of mouse embryos and activation
 A;Reference number: JC5410; MUID:97224429; PMID:9070890
 A;Accession: JC5410
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-277 <MUK>
 A;Cross-references: DDBJ:D86352
 A;Experimental source: embryo
 C;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 18.7%; Score 408; DB 2; Length 277;
 Best Local Similarity 32.1%; Pred. No. 3.2e-27;
 Matches 88; Conservative 52; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILSMFCGCHGLIINNFCRESGLRTRTGSNIDCEKLRFRFSSLHFMVEYKGLTAK 209
 DB 34 DSSYKMDYPEMGICIIITKNPHKSTGMSRSGTDVDAANLRETGMGLKYEVNRKNDLTR 93
 QY 210 KKNVLLALRLAQDHGALDCCVVVILSHGCGQASHLOFPGAVYGTGCPVSEKIVNIFNG 269


```

4 DRSLERNIMFSSHLKVDLEILVIAKQVLNSDNGMIN--SCGTREKREIVKAVQ 61
64 TRGSQALPLFISCLEDTGQDMLASFRL-----TWROAGKLS--- 99
62 RRGDAVAFADYDALRSTGHEGLAEVLEPLARSVDNSNAVEFECFPMSPASHRRSRLSPAGY 121
100 -KPT-----LENITPVVLPEIRK-----PEVLRPETERPVD 130
122 TSPTRVHRDSVSSVSTFYQDIYSRARSRSRSLHSSDRHNSYSPVNAFPSPSSAN 181
131 IGSQGFCDVGALES-----LRGNADLAYILSME-----PC 160
182 SSTGCGSSLYSSRRNRFSKASGPTQYIFHEDMNFVDAPITSRVDEKTYRNFSSGR 241
161 GHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHPMVEVKGDLTAKOMVLALLELA 220
242 GMCLIIINNEHF---EOMPTRNKTKAKDNLNLFRCMGVTICKENLTGRGMULLTIROFA 298
221 R-QCHGALDCCVVVLSHGCOASHLQFPGAVGTCGCPVSEKIVNIFNGTSCPSLGKRP 279
299 KHESHG--DSAILVILSHGEE-----NVIIQVCDIPISTHEIYDILLNAANAPRLANKP 349
280 KLFFIOACQGEQKHGHFEVASTSPEDSPG---SNPEPDATPFQEGRLTFDQDAI- 332
350 KIVFVQACRGERRDNGFPVLDS--VDGVPAFLP-GMDNRDGLFNLGCVR--PQVQVW 405
333 SSLPTSDIFVSYSTPFGFVSWRDPKSGWYVETLNDIFEQWASHEDLOSLLLRVANVS 392
406 RKKPSOAILIAYATTAQVYSWRNSARGSWFIOAVCEVFSTHAKMDVVELLT VNKKVA 465

RESULT 11
B54821
apoptosis regulator ICH-1, suppressive form S - human
C:Species: Homo sapiens (man)
C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A>Title: Ich-1, an ice/ced-3-related gene, encodes both positive and negative regulators
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: B54821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-312 <MAN>
A:Cross-references: GB:U10322
C:Keywords: alternative splicing; apoptosis
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Query Match 13.9%; Score 304; DB 2; Length 312;
Best Local Similarity 29.7%; Pred. No. 3e-18;
Matches 94; Conservative 48; Mismatches 105; Indels 70; Gaps 8;
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```

QY 9 LRRCRLRLVEELQVDMVLLSRELFRPHMIEDIO-RAGSGRRDQARQLIIDLETRGS 67
DB 9 LKQNRVVLAKQLLSLEHLEKDIITLEMRELQAKVGSFS---QNVELLNLLPKRGP 65
QY 68 QALPLFISCLEDTGQDMLASFRLTN-----RQAGKL 98
DB 66 QAFDAFCEALRETKQGHLEDMULLTLISGLQHLVPLPLSCDYDLSLFPVCESCPLYKRL 125
QY 99 SKPTLENLT-----PVVLRLPEIRKPEVLRPETERPVDIGSGFGDVGALSLRGHADLAY 153
DB 126 STDTVEHSLDNKDGVPCLQ-----VKPCTP-----EFYQTHQLAY 161
QY 154 ILSMEPCGHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHPMVEVKGDLTAKOMV 213
DB 162 RLQSRPRGLALVLSNVHFTGKELEFRSGGDVHDSTLTFLFKLLGDYDVHVLCDQTAQEMQ 221
QY 214 LALLELAR-QDHGALDCCVVVLSHGCOASHLQFPGAVGTCGCPVSEKIVNIFNGTSC 272
DB 222 EKLNQFAQLPAHRTVDSICVALLSHGVE-----GATVGDGKLQLOEVEFQLEFDNANC 274
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QY 273 PSLGCKPKLFFIOACGG 289
DB 275 PSLQKPKMFFIOACRG 291
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RESULT 12

A46495

IL-1 beta convertase - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A46495; A47258; I48911

R:Nett, M.A.; Cerretti, D.P.; Berson, D.R.; Seavitt, J.; Gilbert, D.J.; Jenkins, N.A.;

J. Immunol. 149, 3254-3259, 1992

A>Title: Molecular cloning of the murine IL-1 beta converting enzyme cDNA.

A:Reference number: A46495; MUID:93056487; PMID:1431103

A:Accession: A46495

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-402 <NET>

A:Cross-references: GB:I03799; NID:gi198379; PIDN:AAA39306.1; PID:gl198380

A>Note: sequence extracted from NCBI backbone (NCBIP:117473)

R:Molineaux, S.M.; Casano, F.J.; Rolando, A.M.; Peterson, E.P.; Limjuco, G.; Chin, J.;

ard, A.D.; Thornberry, N.A.; Kostura, M.J.

Proc. Natl. Acad. Sci. U.S.A. 90, 1809-1813, 1993

A>Title: Interleukin 1 beta (IL-1 beta) processing in murine macrophages requires a str

A:Reference number: A47258, MUID:93189587; PMID:8446594

A:Accession: A47258

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-187, 189-402 <MOL>

A:Experimental source: macrophage

A>Note: sequence extracted from NCBI backbone (NCBIP:126931)

R:Casano, F.J.; Rolando, A.M.; Mudgett, J.S.; Molineaux, S.M.

Genomics 20, 474-481, 1994

A>Title: The structure and complete nucleotide sequence of the murine gene encoding int

A:Reference number: A54264; MUID:94307735; PMID:8034321

A:Accession: I48911

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 'MAN', 7-402 <RES>

A:Cross-references: EMBL:U04269; NID:9476217; PIDN:AAAS6992.1; PID:9476218

C:Genetics:

A:Introns: 6/1; 92/1; 113/1; 150/3; 208/3; 287/1; 334/1; 370/3

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Query Match 12.3%; Score 268.5; DB 2; Length 402;
Best Local Similarity 24.7%; Pred. No. 4.7e-15;
Matches 110; Conservative 62; Mismatches 183; Indels 91; Gaps 16;
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QY 7 RLRCRLRLVEELQ---VDQLMDVLLSRELFRPHMIEDIO-RAGSGRRDQARQLIIDLE 63
DB 4 KILRAKQKQFINSVSIGTINGLLDELEKRVLNQEMDKILANI-TAMDKARDLCDHVS 62
QY 64 TRGSQALPLFIS---CLEDTGQDMLASFRL-----RTN 92
DB 63 KKGPOASQIFITVICNEDC---YLAGILEQSAPSAETPVATEDSKGHPSSSETKEQN 119
QY 93 ROAGKLSKPTLENLTPVLRPEIRKPEVLRPETERPVDIGSGFGDVGALSLRGHADLAY 152
DB 120 KEDG-----TFPGLTGTLKFCPLKAKLWKENP-----SEIYPIMNTTTRTLA 164
QY 153 YILSMEPCGHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRFSLHPMVEVKGDLTAKOM 212
DB 165 -----LIIICNTEF---OHLSPRVCAQVDLREMKLLLEDGLYTVKVENLTALAM 210
QY 213 VLALLELAR-QDHGALDCCVVVLSHGCOASHLQFPGAVGTCGCPV-SVEKIVNIFNGT 270
DB 211 VKEVKGFACPEHKTSDSSTFLVPMSHGIOEG---ICGTTYSNEVSDILKVOTIFOMNTL 267
QY 271 SCPSLAGCKPKLFFIOACGGEQKHGHFEVASTSPEDSPGNSPEPDATPFQEGRLT---FD 327
DB 268 KCFSLKDKPKVIIIOACRGKQ--GVVLLKDSVRDS-----EEDFLTDALIFE 312
QY 328 QLDIAISSLPTSPDIFVSYSTFPFGFVSWRDPKSGWYVETLDDIFEQWASHEDLOSLLLRV 387
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,Molecule type: protein
;Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
;Genetics:
;Gene: GDB:IL1BC
;Cross-references: GDB:132368; OMIM:147678
;Map position: 11q23-11q23
;Keywords: cysteine proteinase; hydrolase

Query Match      11.9%; Score 259; DB 2; Length 404;
Best Local Similarity 24.3%; Pred. No. 3.1e-14;
Matches 104; Conservative 62; Mismatches 176; Indels 86; Gaps 14;

y 10 RCRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRDQARQLIIDLETGSOA 69
b 10 RKLFIRSMGGGTINGLLDELLQTRVLNKEEMKVKRE-NATVMDKTRALIDSIPKGAQA 68
y 70 LPLFIS--CLED-----TGQDMLASFRTNRCAGKLSKPTLENLTPVLRPEIRKP 118
b 69 COICITY:CEEDSYLACTGLGSADOTSGNYLNMQDSOGVLS-----SFPAP 114
y 119 EVLRPETPRVDIGSGFGVGVALES-----RGNADLAYILSMPCGH-CLIIINNVPFC 172
b 115 QAVODNPAMPTSSGSEGNVKKLSLEEAQRIWKOKSAEIIYPIMDKSRTLRALIIICNEEF- 173
y 173 RESGLRTRTGSNIDCEKLRRRFFSLHFMEVK--AKKVVLLALLELA-RQDHGALDCCV 231
b 174 --DSIPRTGAEDVITGTMLLQLNLGYSDVYK TASDMTTELEAPAPRPEKTSDSSTF 231
y 232 VVILSHG-----COASHL-QPPGAVYGTGCPV--EXIVNIFNGTSCPSLGKPKLFFIQ 285
b 232 LVFMSHGIREGICGKKHSEQVPI-----LNALFNMLNTKNCPSLKDKPKVILIIQ 283
y 286 ACCGEQKHGFEVASTSPDESP-----GSNPEPDATPFOEGLRTFDQIDALS 333
b 284 ACRG-----DSPGVVWFKDSVGVSGNLSLPTTTEEPED-----DAIK 319
y 334 SLPTPSDIFVSYSTFPGFVSMRDPKSGSWVYVETLDDIFEQWAhSEDLSQLLLRVANAVSV 393
b 320 KAHIEKDFIAFCSTPDNVSMWRHPTMGSVFGRLEIHMQEVACSDVEEIFRKVRFSEFQ 379
y 394 KGIYKQMP 401
b 380 PDGRAQMP 387

Search completed: October 20, 2003, 12:14:15
Job time : 45 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

3M protein - protein search, using sw model

run on: October 20, 2003, 12:21:37 ; Search time 99 Seconds
(without alignments)
1084.342 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 416

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNLRKKJFFKTS 416

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 930525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	6.7	393	11 Q9R0S9	Q9R0S9 mus musculus
2	28	6.7	453	11 Q8C3Q0	Q8C3Q0 mus musculus
3	28	6.7	454	11 Q9JHK1	Q9JHK1 rattus norv
4	28	6.7	454	11 Q9R0T0	Q9R0T0 mus musculus
5	28	6.7	454	11 Q8C3Q9	Q8C3Q9 mus musculus
6	26	6.2	383	11 Q99M88	Q99M88 rattus norv
7	20	4.8	177	11 Q920G4	Q920G4 rattus norv
8	17	4.1	403	13 Q90WU0	Q90WU0 gallus gall
9	11	2.6	280	13 Q8JGM9	Q8JGM9 fugu rubrip
10	11	2.6	280	13 Q8JG42	Q8JG42 fugu rubrip
11	11	2.6	280	13 Q8JIS9	Q8JIS9 oryzae lat
12	11	2.6	282	13 Q98U18	Q98U18 brachydanio
13	11	2.6	282	13 Q93417	Q93417 gallus gall
14	11	2.6	290	13 Q8JIS8	Q8JIS8 oryzae lat
15	11	2.6	293	5 Q819V7	Q819V7 bombyx mori
16	11	2.6	299	5 Q81955	Q81955 spodoptera

RESULT 1

Q9R0S9 PRELIMINARY; PRT; 393 AA.
ID Q9R0S9 (TrEMBLrel. 13, Created)
AC Q9R0S9; (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase9S.
GN CASP9.

ALIGNMENTS

Q91b65 xenopus lae
Q81tp2 branchiosto
Q88550 rattus norv
Q9nhf9 drosophila
Q9vet9 drosophila
Q918j3 brachydanio
Q8wyg8 homo sapien
Q91b62 xenopus lae
Q8iup5 homo sapien
Q22518 caenorhabdi
Q942f3 oryza sativ
Q91j13 arabidopsis
Q22476 arabidopsis
Q81t85 vibrionphage
Q8h436 oryza sativ
Q970w7 sulfolobus
Q8yax5 bruceella me
Q9xax4 streptomyce
Q9kuw7 vibrio chol
Q8fxg8 bruceella su
Q91b63 xenopus lae
Q91b67 xenopus lae
Q8kpx0 saccharopol
Q21026 caenorhabdi
Q22203 caenorhabdi
Q48847 arabidopsis
Q18107 caenorhabdi
Q9vax8 drosophila
Q962h8 toxoplasma
Q81899 lycopersico
Q8guq5 lycopersico
Q9exm1 escherichia
Q8y1m1 anabaena sp
Q924c6 salmonella
Q8bn21 mus musculus
Q8bq00 mus musculus
Q9zan6 comamonas s
Q9b4y3 graemye gri
Q9n9c1 leishmania
Q53304 mycoplasma
Q8eqk6 oceanobacil
Q997t2 oryza sativ
Q91mm8 lumpy skin
Q81tp4 lumpy skin
Q81t23 lumpy skin
Q8dc79 vibrio vuln
Q9fgl8 cyanophora
Q8f2w8 leptospira
Q8bpu8 mus musculus
Q81la4 datura fero
Q81tp9 pyrobaculum
Q8gr30 streptomyce
Q8dcy3 vibrio vuln
Q9tim9 bacterioph
Q8ha36 bacterioph
Q9kxf5 escherichia
Q54673 streptomyce
Q58886 pyrococcus
Q23341 arabidopsis

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20011956; PubMed=10529400;
RX Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
RL caspase-9.";
RL Biochem. Biophys. Res. Commun. 264:550-555 (1999).
DR EMBL; AB019601; BAA86896.1;
DR HSSP; P42574; IPAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002198; ICE.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02026; CASPASE_P20; 1.
SQ SEQUENCE 393 AA; 42975 MW; CA899475E5D0D632 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 4 20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 CPSLGKPKLFFIOACGGEQKHGFEVA 299
Db 310 CPSLGKPKLFFIOACGGEQKHGFEVA 337

RESULT 2
Q8C300 PRELIMINARY; PRT; 453 AA.
AC Q8C300;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase 9 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK085152; BAC39378.1; -.
DR NON_TER 1
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA68F CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 4 20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 CPSLGKPKLFFIOACGGEQKHGFEVA 299
Db 309 CPSLGKPKLFFIOACGGEQKHGFEVA 336

RESULT 3
Q9JHK1 PRELIMINARY; PRT; 454 AA.
AC Q9JHK1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-9 (Caspase-9 long isoform).
GN RNCASP9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SPRAGUE-DAWLEY;
RX Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RL in Neuronal Cell Death During Brain Development and Transient Cerebral
RN Ischemia.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=SPRAGUE-DAWLEY;
RX Itoh T., Itoh A., Pleasure D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RX Cao G., Chen D., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RL in Neuronal Cell Death During Brain Development and Transient Cerebral
RN Ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RL Apoptosis.";
RL J. Biol. Chem. 276:12190-12200 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=WKY;
RX MEDLINE=21552893; PubMed=11695991;
RA Niehiyama J., Yi X., Venkatachalam M.A., Dong Z.;
RT "cDNA cloning and promoter analysis of rat caspase-9.";
RL Biochem. J. 360:49-56 (2001).
DR EMBL; AF262319; AAF85658.1; -.
DR EMBL; AF271996; AAF76217.1; -.
DR EMBL; AF286006; AAF99705.1; -.
DR EMBL; AF308469; AAK35159.1; -.
DR EMBL; AY027667; AAK26235.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.010; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50399 MW; 501623B29E6ED6FC CRC64;
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Best Local Similarity 100.0%; Pred. No. 4,6e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Indels 0; Gaps 0;
QY 272 CPSLGGKPKLFFFIQACGGEQKHGFVEA 299
DB 310 CPSLGGKPKLFFFIQACGGEQKHGFVEA 337

RESULT 4
Q9R0T0 PRELIMINARY; PRT: 454 AA.
ID Q9R0T0
AC Q9R0T0
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE CASPase 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
caspase-9".
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
DR EMBL; AB019600; RA08695.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -;
DR MGD; MGI:1277950; Casp9.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50051 MW; 4614989AF823850F CRC64;

Query Match 6.7%; Score 28; DB 11; Length 454;
Best Local Similarity 100.0%; Pred. No. 4,6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 272 CPSLGGKPKLFFFIQACGGEQKHGFVEA 299
DB 310 CPSLGGKPKLFFFIQACGGEQKHGFVEA 337

RESULT 5
Q8C3Q9 PRELIMINARY; PRT: 454 AA.
ID Q8C3Q9
AC Q8C3Q9
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DE CASPase 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK085095; BAC39365.1; -;
SQ SEQUENCE 454 AA; 49979 MW; 438A67EA6A6EE78 CRC64;

Query Match 6.7%; Score 28; DB 11; Length 454;
Best Local Similarity 100.0%; Pred. No. 4,6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 272 CPSLGGKPKLFFFIQACGGEQKHGFVEA 299
DB 310 CPSLGGKPKLFFFIQACGGEQKHGFVEA 337

RESULT 6
Q99M88 PRELIMINARY; PRT: 383 AA.
ID Q99M88
AC Q99M88
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-9 CTD isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
Apoptosis";
RL J. Biol. Chem. 276:12190-12200(2001).
DR EMBL; AY008275; AAC21690.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -;
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 383 AA; 42319 MW; 3C5D217C3100FF25 CRC64;

Query Match 6.2%; Score 26; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 4,8e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 VVILSHGCGQASHLQFPFGAVYGTDC 256
DB 269 VVILSHGCGQASHLQFPFGAVYGTDC 294

RESULT 7
Q920G4 PRELIMINARY; PRT: 177 AA.
ID Q920G4
AC Q920G4
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Caspase-9 short form.
OS Rattus norvegicus (Rat).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Chen D., Ma L., Graham S.H., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF293333; AAK97056.1;
DR InterPro: IPR001315; CARD;
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS50209; CARD; 1.
SQ SEQUENCE 177 AA; 19700 MW; E9DCDA77156AD748 CRC64;

Query Match 4.88; Score 20; DB 11; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 MIEDIQAGSGRRDQARQL 58
Db 39 MIEDIQAGSGRRDQARQL 58

RESULT 8
Q90WUO ID Q90WUO PRELIMINARY; PRT; 403 AA.
AC Q90WUO
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC Barton S., Bridgham J.T., Johnson A.L.;
RA "Caspase-8 and -9 expression in the hen ovary.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY057940; AAL23701.1;
DR InterPro: IPR001315; CARD;
DR InterPro: IPR002138; ICE;
DR InterPro: IPR001309; ICE_P10.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBENZYME.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR NON TER 1
FT SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 4.18; Score 17; DB 13; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFIQAGGQK 293
Db 264 GKPKLFFIQAGGQK 280
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RESULT 9
Q8JGM9 ID Q8JGM9 PRELIMINARY; PRT; 280 AA.
AC Q8JGM9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase 3-like.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
CX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Hewitt J.E., Bolland D.J.;
RT "Sequence comparisons of an evolutionary chromosomal breakpoint in
RT human, mouse and pufferfish.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY102865; AAM48291.1;
DR InterPro: IPR002138; ICE;
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBENZYME.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 280 AA; 30538 MW; 4D58912159A37347 CRC64;

Query Match 2.68; Score 11; DB 13; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFIQAC 287
Db 159 GKPKLFFIQAC 169

RESULT 10
Q8JG42 ID Q8JG42 PRELIMINARY; PRT; 280 AA.
AC Q8JG42
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase 3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
CX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97311173; PubMed=9166581;
RA Grewal P.K., van Deutekom J.C., Mills K.A., Lemmers R.J.,
RA Mathews K.D., Frants R.R., Hewitt J.E.;
RT "The mouse homolog of FRG1, a candidate gene for FSHD, maps proximal
RT to the myodystrophy mutation on chromosome 8.";
RL Mamm. Genome 8:394-398 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=98382568; PubMed=9714712;
RA Grewal P.K., Todd L.C., van der Maarel S., Frants R.R., Hewitt J.E.;
RT "FRG1, a gene in the FSH muscular dystrophy region on human chromosome
RT 4q35, is highly conserved in vertebrates and invertebrates.";
RN [2]
```


Gene 216:13-19(1998).
 [3]
 SEQUENCE FROM N.A.
 MEDLINE=21303262; PubMed=11410364;
 Bolland D.J., Hewitt J.E.;
 "Intron loss in the SARTI genes of Fugu rubripes and Tetraodon
 nigroviridis";
 Gene 271:43-49(2001).
 [4]
 SEQUENCE FROM N.A.
 Bolland D.J., van Geel M., Carim Todd L., Grewal P.K., Beck A.F.,
 van der Maarel M. Sr., Frants R.R., de Jong P.J., Hewitt J.E.;
 "Sequence Comparisons of an Evolutionary Chromosomal Breakpoint in
 Human, Mouse and Puffer Fish";
 Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AF042797; AAM43816.1; -
 InterPro: IPR002398; ICE.
 InterPro: IPR002138; ICE_p10.
 InterPro: IPR001309; ICE_p20.
 Pfam: PF00655; ICE_p10; 1.
 Pfam: PF00656; ICE_p20; 1.
 PRINTS; PR00376; IL1BCENZME.
 SMART; SM00115; CASC; 1.
 PROSITE; PS01122; CASPASE_CYS; 1.
 PROSITE; PS01121; CASPASE_HIS; 1.
 PROSITE; PS0207; CASPASE_P10; 1.
 PROSITE; PS0208; CASPASE_P20; 1.
 SEQUENCE 280 AA; 30524 MW; 4F2D91245A:E:642 CRC64;
 Query Match 2.6%; Score 11; DB 13; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GKPKLFFIQAC 287
 DB 159 GKPKLFFIQAC 169
 [11]
 RESULT 11
 ID Q8JIS9 PRELIMINARY; PRT; 280 AA.
 AC Q8JIS9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Caspase 3B.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziatryzias.
 NCBI_TaxID=8090;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=20211495; PubMed=10747068;
 Naruse K., Fukumachi S., Mitani H., Kondo T., Matsuo T., Kondo S.,
 Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
 Wada H., Kusabe T., Suzuki N., Kinoshita M., Kanamori A., Terada T.,
 Kimura H., Nonaka M., Shima A.;
 "A Detailed Linkage Map of Medaka, Oryzias latipes: Comparative
 Genomics and Genome Evolution";
 Genetics 154:1773-1784(2000).
 EMBL; AB032608; BAC00948.1; -
 InterPro: IPR002398; ICE.
 InterPro: IPR002138; ICE_p10.
 InterPro: IPR001309; ICE_p20.
 Pfam: PF00655; ICE_p10; 1.
 Pfam: PF00656; ICE_p20; 1.
 PRINTS; PR00376; IL1BCENZME.
 SMART; SM00115; CASC; 1.
 PROSITE; PS01122; CASPASE_CYS; 1.
 PROSITE; PS01121; CASPASE_HIS; 1.
 PROSITE; PS0207; CASPASE_P10; 1.
 PROSITE; PS0208; CASPASE_P20; 1.

DR PROSITE; PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 31168 MW; 5095512F1E485542 CRC64;
 Query Match 2.6%; Score 11; DB 13; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GKPKLFFIQAC 287
 DB 160 GKPKLFFIQAC 170
 [11]
 RESULT 12
 ID Q98UI8 PRELIMINARY; PRT; 282 AA.
 AC Q98UI8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Caspase-3.
 GN CASP3.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yabu T., Okazaki T., Yamashita M.;
 "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
 Mammalian Caspase-3";
 Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 EMBL; AB047003; BAB32409.1; -
 DR HSSP; P42574; IPAU.
 DR MEROPS; C14.003; -
 DR ZFIN; ZDB-GENE-011210-1; casp3.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; IL1BCENZME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;
 Query Match 2.6%; Score 11; DB 13; Length 282;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GKPKLFFIQAC 287
 DB 156 GKPKLFFIQAC 166
 [11]
 RESULT 13
 ID O93417 PRELIMINARY; PRT; 283 AA.
 AC O93417;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Caspase-3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 [1]
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20149872; PubMed=10684799;
 RA Johnson A.L., Bridgham J.T.:
 RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
 cells.";
 RL Biol. Reprod. 62:589-598(2000).
 DR EMBL: AF083029; AAC32602.1; --
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.003; --
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; IL1BCNZYME.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFFD4DC4F CRC64;

Query Match 2.6%; Score 11; DB 13; Length 283;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287

Db 161 GKPKLFFFIQAC 171

RESULT 14

Q8JIS8 PRELIMINARY; PRT; 290 AA.
 AC Q8JIS8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Caspase 3A.
 OS Oryzias latipes (Medaka fish) (Japanese reefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20211495; PubMed=10747068;
 RA Natuse K., Fukamachi S., Mitani H., Kondo S., Matsuo K., Kondo S.,
 RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
 RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terada T.,
 RA Kimura H., Nonaka M., Shima A.;
 RT "A Detailed Linkage Map of Medaka, Oryzias latipes: Comparative
 RT Genomics and Genome Evolution.";
 RL Genetics 154:1773-1784(2000).
 DR EMBL: AB032609; BAC00949.1; --
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; IL1BCNZYME.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 290 AA; 32686 MW; D8C3BC00D32E8A6C CRC64;

Query Match 2.6%; Score 11; DB 13; Length 290;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287

Db 166 GKPKLFFFIQAC 176

RESULT 15

Q819V7 PRELIMINARY; PRT; 293 AA.
 ID Q819V7;
 AC Q819V7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Caspase-1.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22358983; PubMed=12324475;
 RA Pei Z., Reske G., Huang Q., Hammock B.D., Qi Y., Chejanovsky N.;
 RT "Characterization of the Apoptosis Suppressor Protein p49 from the
 RT Spodoptera littoralis Nucleopolyhedrovirus.";
 RL J. Biol. Chem. 277:48677-48684(2002).
 DR EMBL: AF48494; AAN86250.1; --
 SQ SEQUENCE 293 AA; 33340 MW; 8184A9FD910D7E34 CRC64;

Query Match 2.6%; Score 11; DB 5; Length 293;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287

Db 165 GKPKLFFFIQAC 175

RESULT 16

Q81955 PRELIMINARY; PRT; 299 AA.
 ID Q81955;
 AC Q81955;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Effector caspase.
 OS Spodoptera littoralis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
 OC Noctuidae; Amphipyriinae; Spodoptera.
 OX NCBI_TaxID=7109;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Q., Gershburg E., Qi Y., Chejanovsky N.;
 RT "Suppression of apoptosis in Spodoptera littoralis SL2 cells by the
 RT baculovirus proteins P35 and P49.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF548387; AAO16241.1; --
 SQ SEQUENCE 299 AA; 33442 MW; B13AF2C1AGBD409D CRC64;

Query Match 2.6%; Score 11; DB 5; Length 299;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287

Db 168 GKPKLFFFIQAC 178

RESULT 17

Q91B65 PRELIMINARY; PRT; 318 AA.
 ID Q91B65;
 AC Q91B65;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase-7.
GN XCASPASE-7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038170; BAA94748.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -;
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002398; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 318 AA; 35937 MW; 6ERC6684AF8A128 CRC64;

Query Match 2.6%; Score 11; Ds 13; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.01c; 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 277 GKPKLFFIOAC 287
|||||
DB 187 GKPKLFFIOAC 197

RESULT 18
Q81TP2 PRELIMINARY; PRT; 400 AA.
ID Q81TP2
AC Q81TP2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AmphicASP-6.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA Bayascas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,
RA Comella J.X.;
RT "Isolation of AmphicASP-6, an amphioxus (Branchiostoma floridae)
caspase-6 homolog containing a Pyrin prodomain";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF412336; AAN45950.1; -;
SQ SEQUENCE 400 AA; 44309 MW; 5C3B1B813E73DFAE CRC64;

Query Match 2.6%; Score 11; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 0.022; 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 277 GKPKLFFIOAC 287
|||||
DB 260 GKPKLFFIOAC 270

RESULT 19
O88550

ID O88550 PRELIMINARY; PRT; 303 AA.
AC O88550;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Forghani F., Roy S.;
RT "Rat caspase-7 sequence";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072124; AAC24011.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -;
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34324 MW; A71728754BF199DD CRC64;

Query Match 2.4%; Score 10; DB 11; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.18; 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 278 KPKLFFIOAC 287
|||||
DB 177 KPKLFFIOAC 186

RESULT 20
Q9NHF9 PRELIMINARY; PRT; 308 AA.
ID Q9NHF9
AC Q9NHF9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase 6-like protein BG2.
GN DECAV OR CG14902.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou L., Steller H.;
RT "BG2, a potential drosophila homologue of Caspase 6";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222007; AAF44327.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.022; -;
DR FlyBase; FBgn0028381; decay.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.

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DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 308 AA; 34897 MW; E3FDAB0DSFEC7E93 CRC64;

Query Match          2.4%; Score 10; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPQLFFFIQAC 287
DB 162 KPQLFFFIQAC 171

RESULT 21
Q9VET9 PRELIMINARY; PRT; 308 AA.
AC Q9VET9;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Decay protein (ATC03047p).
GN DECA1 OR C014902.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoisinger R.A., Galle R.F.,
RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke K., Davenport J.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocua S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischman W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL SEQUENCE 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99452973; PubMed=10521468;
RD Dorstyn L., Read S.H., Quinn L.M., Richardson H., Kumar S.;

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RT "DECAY, a novel Drosophila caspase related to mammalian caspase-3 and
RT caspase-7.",
RL J. Biol. Chem. 274:30778-30783(1999).
[3]
RN SEQUENCE FROM N.A.
RP Dorstyn L., Read S.H., Kumar S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Change M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleeb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003713; AAF55329.1; -
DR EMBL; AF130469; AAD54071.2; -
DR EMBL; AY089242; AAL89980.1; -
DR HSSP; F42574; 1PAJ.
DR MEROPS; C14.022; -
DR FlyBase; FBgn0028381; decay.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p1.
DR Pfam; PF00656; ICE_p2; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASG. 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 308 AA; 34911 MW; 686DA39060EC78C1 CRC64;

Query Match          2.4%; Score 10; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPQLFFFIQAC 287
DB 162 KPQLFFFIQAC 171

RESULT 22
Q918J3 PRELIMINARY; PRT; 476 AA.
AC Q918J3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase-8.
GN CASP8.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Zebrafish",
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF273220; AAF79207.1; -
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.009; -
DR ZFIN; ZDB-GENE-000713-1; casp8.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

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R Pfam: PF01335; DED; 2.
R Pfam: PF00655; ICE_p10; 1.
R Pfam: PF00656; ICE_p20; 1.
R PRINTS: PR00376; IL1BCENZYM.
R SMART: SM00115; CASC; 1.
R SMART: SM00031; DED; 2.
R PROSITE: PS01122; CASPASE_CYS; 1.
R PROSITE: PS50207; CASPASE_P10; 1.
R PROSITE: PS50208; CASPASE_P20; 1.
R PROSITE: PS50168; DED; 2.
Q SEQUENCE 476 AA; 54890 MW; FD9DF4B3C3C1FB9 CRC64;

Query Match 2.4%; Score 10; DB 13; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 278 KPKLFFFIQAC 287
b 346 KPKLFFFIQAC 355

RESULT 23
8WYQ8 PRELIMINARY; PRT; 479 AA.
C Q8WYQ8;
T 01-MAR-2002 (TReMBLrel. 20, Created)
T 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
T 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
E Caspase-10a.
XS Homo sapiens (Human).
XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
XN [1]
RP SEQUENCE FROM N.A.
MEDLINE=21100893; PubMed=11161814;
HADANO S., Yanagisawa Y., Skaug J., Fichte K., Nasir J.,
Martindale D., Koop B.F., Scherer S.W., Ni holson D.W., Rouleau G.A.,
Ikeda J.-E., Hayden M.R.;
"Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
critical region at chromosome 2q33-q34: Candidate genes for ALS2.";
Genomics 71:200-213(2001).
R EMBL: AB038978; BAB32553.1; JOINED.
R EMBL: AB038973; BAB32553.1; JOINED.
R EMBL: AB038974; BAB32553.1; JOINED.
R EMBL: AB038975; BAB32553.1; JOINED.
R EMBL: AB038977; BAB32553.1; JOINED.
R InterPro: IPR001875; DED; 2.
R InterPro: IPR002398; ICE.
R InterPro: IPR002138; ICE_p10.
R InterPro: IPR001309; ICE_p20.
R Pfam: PF01335; DED; 2.
R Pfam: PF00655; ICE_p10; 1.
R Pfam: PF00656; ICE_p20; 1.
R PRINTS: PR00376; IL1BCENZYM.
R SMART: SM00115; CASC; 1.
R SMART: SM00031; DED; 2.
R PROSITE: PS01122; CASPASE_CYS; 1.
R PROSITE: PS01121; CASPASE_HIS; 1.
R PROSITE: PS50207; CASPASE_P10; 1.
R PROSITE: PS50208; CASPASE_P20; 1.
R PROSITE: PS50168; DED; 2.
R SEQUENCE 479 AA; 54565 MW; 1317FD7A4ZE003FF CRC64;

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPKLFFFIQAC 287
Db 349 KPKLFFFIQAC 358

us-09-961-201a-1.oligo.rspt

RESULT 24
Q91B62 PRELIMINARY; PRT; 520 AA.
AC Q91B62;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Caspase-10.
GN XCASPASE-10.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
"Structure, expression and function of the Xenopus laevis caspase
family.";
J. Biol. Chem. 275:10484-10491(2000).
RL EMBL: AB038173; BAA94751.1; -.
DR HSSP; Q15806; IQDU.
DR InterPro: IPR001875; DED.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF01335; DED; 2.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00115; CASC; 1.
DR SMART: SM00031; DED; 2.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS50168; DED; 2.
R SEQUENCE 520 AA; 59626 MW; 331645A09CA6615 CRC64;

Query Match 2.4%; Score 10; DB 13; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPKLFFFIQAC 287
Db 383 KPKLFFFIQAC 392

RESULT 25
Q81UP5 PRELIMINARY; PRT; 522 AA.
AC Q81UP5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Caspase 10, apoptosis-related cysteine protease.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Brain;
RA Strauberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC042844; AAH42844.1; -.
KW Protease.
SQ SEQUENCE 522 AA; 58993 MW; 34847E073DFA688 CRC64;

Query Match 2.4%; Score 10; DB 4; Length 522;
Best Local Similarity 100.0%; Pred. No. 0.31;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 278 KPKLFFIQAC 287
b 392 KPKLFFIQAC 401

RESULT 26
122518 PRELIMINARY; PRT; 370 AA.
D Q22518
C Q22518;
T 01-NOV-1996 (TEMBLrel. 01, Created)
Y 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
Y 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
E T15B12.2 protein.
N T15B12.2.
S Caenorhabditis elegans.
C Eukaryota; Metazoa; Nematoda; Chromadorea; R: ditida; Rhabditoides;
X Rhabditidae; Peloderinae; Caenorhabditis.
X NCBI_TaxID=6239;
N [1]
R SEQUENCE FROM N.A.
R STRAIN=Bristol N2;
R Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
R Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
R Craxton M., Dear S., Du Z., Duthin R., Falo A., Fulton L.,
R Gardner A., Green P., Hawkins T., Hillier J., Jier M., Johnston L.,
R Jones M., Kersey J., Kirtlen J., Laister J., Latreille P.,
R Lightning J., Lloyd C., McMurray A., Mortimer B., O'Callaghan M.,
R Parsons J., Percy C., Rifkin L., Roop A., Saunders D., Showkneen R.,
R Snelson N., Smith A., Sonhammer E., Stadler R., Sulston J.,
R Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
R Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
R "The C. elegans genome project: Contiguous nucleotide sequence of over
R two megabases from chromosome III."
R Nature 0:0-0(1994).
R [2]
R SEQUENCE FROM N.A.
R STRAIN=Bristol N2;
R Talch A.;
R Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
R [3]
R SEQUENCE FROM N.A.
R STRAIN=Bristol N2;
R Waterston R.;
R Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
R CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
R EMBL; U14634; AAA21560.1; -.
R HSP; O06486; 1CKJ.
R WormPep; T15B12.2; CE01404.
R InterPro; IPR000719; Prot_kinase.
R InterPro; IPR002290; Ser_Thr_pkinase.
R Pfam; PF00069; pkinase; 1.
R ProDom; PD000001; Prot_kinase; 1.
R PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
R SQ SEQUENCE 370 AA; 42308 MW; A485A7DCC6FB7599 CRC64;

Query Match 2.2%; Score 9; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSFGFGDV 139
DB 57 IGSFGFGDV 65
|||||
SEQUENCE FROM N.A.

RESULT 27
Q942F3 PRELIMINARY; PRT; 1121 AA.
AC Q942F3;

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DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Putative brassinosteroid-insensitive protein BRIL.
GN P0480C01.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT *Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0480C01.13.
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AP003453; BAB68053.1; -.
DR Gramene; Q942F3; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007030; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00560; LRR; 14.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS05052; LRR_PS; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
R SQ SEQUENCE 1121 AA; 120180 MW; F71A49B45E0E2D09 CRC64;

Query Match 2.2%; Score 9; DB 10; Length 1121;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSFGFGDV 139
DB 813 IGSFGFGDV 821
|||||
SEQUENCE FROM N.A.

RESULT 28
Q9LJF3 PRELIMINARY; PRT; 1164 AA.
AC Q9LJF3;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Receptor protein kinase (ATG13380/MRP15_1).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosida II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT *Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety Pl.
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
RN [3]
RP SEQUENCE FROM N.A.

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RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Iehida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Tokiomi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AP00603; BAB01743.1; -;
 DR EMBL; AV128280; AAM91089.1; -;
 DR InterPro; IPR001611; LRR;
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00560; LRR; 20.
 DR Pfam; PF00560; pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS05052; LRR_PS; 5.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 1164 AA; 126660 MW; 79380581D100EEEC CRC64;
 SQ

Query Match 2.2%; Score 9; DB 10; Length 1164;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSFGFGDV 139
 |||||
 DB 864 IGSFGFGDV 872

RESULT 29
 ID 022476 PRELIMINARY; PRT; 1196 ;
 AC 022476;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Brassinosteroid insensitive 1 (Brassinosteroid insensitive 1 gene) (BR11).
 DE BR11 OR F23K16.30 OR AT4G39400.
 GN GN
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 (1)
 SEQUENCE FROM N.A.
 RP STRAIN=cv. COL-C;
 RC MEDLINE=97442355; PubMed=92989904;
 RA Li J., Chory J.;
 RT "A putative leucine-rich repeat receptor kinase involved in
 RT brassinosteroid signal transduction.";
 RL Cell 90:929-938(1997).
 (2)
 SEQUENCE FROM N.A.
 RP Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 (3)
 SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 (4)
 SEQUENCE FROM N.A.
 RP Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 (5)
 SEQUENCE FROM N.A.
 RP EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF017056; AAC49810.1; -;
 DR EMBL; AL078620; CAB44675.1; -;
 DR EMBL; AL161595; CAB80603.1; -;
 DR InterPro; IPR001611; LRR;
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00560; LRR; 20.
 DR Pfam; PF00560; pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS05052; LRR_PS; 5.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1196 AA; 130542 MW; C7FBA1C21294E600 CRC64;
 Query Match 2.2%; Score 9; DB 10; Length 1196;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSFGFGDV 139
 |||||
 DB 889 IGSFGFGDV 897

RESULT 30
 ID 08LT85 PRELIMINARY; PRT; 145 AA.
 AC 08LT85;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Vibriophaga VpV262.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC T7-like viruses.
 OC NCBI_TaxID=194802;
 (1)
 SEQUENCE FROM N.A.
 RA Hardies S.C.;
 RT "The complete sequence of Vibriophaga VpV 262.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY095314; AAM28362.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 145 AA; 16341 MW; 7989720F8C1B998 CRC64;
 Query Match 1.9%; Score 8; DB 9; Length 145;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LARQDHGA 226
 |||||
 DB 14 LARQDHGA 21

RESULT 31
 ID 08H436 PRELIMINARY; PRT; 158 AA.
 AC 08H436;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE P0407H12.33 protein.

3N P0407H12.33.
 3S Oryza sativa (japonica cultivar-group).
 3C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 3C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 3C Ehrhartoideae; Oryzaceae; Oryza.
 3X NCBI_TaxID=39947;
 3R [1]
 3P SEQUENCE FROM N.A.
 3R STRAIN=cv. Nipponbare;
 3A Sasaki T., Matsumoto T., Yamamoto K.;
 3R "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
 3T clone:p0407h12";
 3R Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 3R EMBL: AP004303; BAC21455.1; ...
 3R SEQUENCE 158 AA; 17275 MW; AAD0FB7E5BA02983 CRC64;

Query Match 1.9%; Score 8; DB 10; Length 158;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LRRCLRL 16
 54 LRRCLRL 6;
 1111111111

RESULT 32

Q970W7 PRELIMINARY; PRT; 165 AA.
 AC Q970W7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein ST1485.
 GN ST1485.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RK PubMed=1157479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Rep. 8:123-140(2001).
 DR EMBL: AP000986; BAB6556.1;
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 165 AA; 19200 MW; 4A39578B3CCA2400 CRC64;

Query Match 1.9%; Score 8; DB 17; Length 165;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALESRLGN 148
 99 ALESRLGN 106
 1111111111

RESULT 33

Q8VAX5 PRELIMINARY; PRT; 324 AA.
 AC Q8VAX5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Oxidoreductase (EC 1.1.1.-).
 GN BME111126.

OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapratl V., Redkar R.J., Patra G., Mujer C., Loe T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009744; AAL54368.1;
 DR InterPro: IPR000683; GFO_IDH_MoCA.
 DR Pfam: PF01408; GFO_IDH_MoCA; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 324 AA; 35683 MW; 3817F865ABDA4:12 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 324;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARO 222
 103 ALLELARO 110
 1111111111

RESULT 34

Q9XAC4 PRELIMINARY; PRT; 368 AA.
 ID Q9XAC4;
 AC Q9XAC4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SC01932.
 GN SC01932 OR SC22.14C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seger K., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
RL EMBL; AL939110; CAB50757.1; -;
DR InterPro; IPR000209; Peptidase_S8.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 368 AA; 38767 MW; DBF94549F6303FF0 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 368;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EADRLRLR 10
DB 81 EADRLRLR 88
|||||

RESULT 35
Q9KUM7 PRELIMINARY; PRT; 372 AA.
AC Q9KUM7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amino transferase, class V.
GN VC0392.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
CX NCBI_TaxID=666;

[1]
SEQUENCE FROM N.A.
RN STRAIN=El Tor N16961 / Serotype O1;
RC MEDLINE=20406833; PubMed=109523101;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Winn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., McAlano J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RL EMBL; AE004127; AAF93565.1; -;
DR TIGR; VC0392;
DR InterPro; IPR000192; Amino transferase.
DR Pfam; PF00266; aminotran_5; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
DR Transferase; Complete proteome.
SQ SEQUENCE 372 AA; 40623 MW; 00D5AFD1B6F6947B CRC64;

Query Match 1.9%; Score 8; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCPVSVEK 262
DB 119 GCPVSVEK 126
|||||

RESULT 36
Q8FXG8 PRELIMINARY; PRT; 378 AA.
AC Q8FXG8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Oxidoreductase, Gco/Idh/MocA family.

GN BRA0109.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RC MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
RL EMBL; AE014514; AAN33319.1; -;
DR TIGR; BRA0109; -;
KW Complete proteome.
SQ SEQUENCE 378 AA; 41413 MW; 7F53CB96065F3787 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 378;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
DB 103 ALLELARQ 110
|||||

RESULT 37
Q9IB63 PRELIMINARY; PRT; 399 AA.
AC Q9IB63;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-9.
GN XCASPA9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

[1]
SEQUENCE FROM N.A.
RN MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -;
DR HSSP; Q15806; IQDU.
DR MEROPS; C14.010; -;
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.

OX	NCBI_TaxID=1836;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=CA340;
RA	Luz-Madrigal A., Petrosyan P., De la Torre P., Flores M.E.;
RC	"Saccharopolyspora erythroa genomic DNA comprising methylmalonyl-CoA
RT	mutase operon";
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
DR	EMBL; AY117133; AAC77044.1; --
DR	InterPro; IPR006099; MMCoA_mutase.
DR	Pfam; PF01642; MM CoA mutase; 1.
SQ	SEQUENCE 618 AA; 66044 MW; 7E8E3B3A4D91CBE1 CRC64;
Query Match	1.9%; Score 8; DB 2; Length 618;
Best Local Similarity	100.0%; Pred.No.44;
Matches	8; Conservative C; Mismatches 0; Indels 0; Gaps
QY	360 GSYYVETL 367
Db	386 GSYYVETL 393
RESULT 40	
Q21026	PRELIMINARY; PRT; 752 AA.
ID	Q21026
AC	Q21026;
DT	01-NOV-1996 (TREMBLrel_01, Created)
DT	01-NOV-1996 (TREMBLrel_01, Last sequence update)
DT	01-MAR-2003 (TREMBLrel_23, Last annotation update)
DE	F59A6.4 protein.
GN	F59A6.4.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC	Rhabditiidae; Peloderinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	MEDLINE-99069613; PubMed=9851916;
RA	None;
RT	"Genome sequencing of the nematode C. elegans: a platform for
RT	investigating biology. The C. elegans Sequencing Consortium.";
RL	Science 282:2012-2018(1998).
RN	[2]
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RA	Nhan M.;
RT	"The sequence of C. elegans cosmid F59A6.";
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBSJ databases.
RN	[3]
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	Waterston R.;
RA	Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR	EMBL; U41994; AAK31524.1; --
DR	HSSP; Q06486; 1CKI
DR	MormRep; F59A6.4; CE01982.
DR	InterPro; IPR000719; Prot_kinase.
DR	Pfam; PRF0069; pkinase; 1.
DR	ProDom; PD00001; Prot_kinase; 2.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
KW	ATP-binding; Transferase.
SQ	SEQUENCE 752 AA; 85325 MW; 34F307B45DE89CFF CRC64;
Query Match	1.9%; Score 8; DB 5; Length 752;
Best Local Similarity	100.0%; Pred.No.53;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	132 GSGGFGDV 139
Db	441 GSGGFGDV 448

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RESULT 41
Q22203 ID Q22203 PRELIMINARY; PRT; 758 AA.
AC Q22203;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 85.8 kDa protein.
DE T05A7.6.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA MEDLINE=99069613; PubMed=9851916;
RX None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:202-208(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Chisoe S.;
RX "The sequence of C. elegans cosmid T05A7."
RT Submitted (NOV-1995) to the EMBL/GenBank/ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RX "Direct Submission."
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; U40028; AAA8115.1; -.
DR HSSP; Q06486; 1CKI.
DR WormPep; T05A7.6; CE04892.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 2.
DR ProDom; PD000001; Prot_kinase; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 2.
DR Hypothetical protein; ATP-binding; Transferase.
KW SEQUENCE 758 AA; 85847 MW; 7A1EDB04D72F6C9B CRC64;

Query Match 1.9%; Score 8; DB 5; Length 758;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
DB 447 GSGGFGDV 454

RESULT 42
O48847 ID O48847 PRELIMINARY; PRT; 787 AA.
AC O48847;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F24L7.16 protein (AT2G32700/F24L7.16).
DE F24L7.16.
GN Arabidopsis thaliana (Mouse-ear cross).
OS Arabidopses thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
```

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RA Somerville C.R., Venter J.C.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC003974; AAC04493.1; -.
DR EMBL; AF367306; AAK32893.1; -.
DR EMBL; BT002219; AAN72230.1; -.
DR InterPro; IPR006594; Lish.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00667; Lish; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00082; WD_REPEATS_2; 5.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 787 AA; 85514 MW; 995B52584090CEC3 CRC64;

Query Match 1.9%; Score 8; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 FGDVGALE 143
DB 456 FGDVGALE 463

RESULT 43
O18107 ID O18107 PRELIMINARY; PRT; 794 AA.
AC O18107; O62283;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE H05L14.1 protein.
DE H05L14.1.
GN Caenorhabditis elegans.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fulton L.,
RA Gardner A., Green P., Hawkes T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kersey J., Kirsten J., Laister N., Latreille P.,
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Lightning J., Lloyd C., McMurray A., Mortimer B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R., Smailson N., Smith A., Sonhammer E., Stader R., Sultson J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J., Wohlman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*." Nature 368:32-38(1994).

RA Nature 368:32-38(1994).

RP SEQUENCE FROM N.A.

RC Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

RA EMBL: Z99772; CAB:3921.1; J. JOINED.

DR EMBL: Z75550; CAB:6921.1; J. JOINED.

DR EMBL: Z75550; CAB:6921.1; J. JOINED.

DR EMBL: Z99772; CAB:3921.1; J. JOINED.

DR HSP: Q06486; ICK1.

DR WormPep: H05L14.1; CE16168.

DR InterPro: IPR000719; Prot_kinase.

DR Pfam: PF00069; pkinase; 2.

DR ProDom: PD000001; Prot_kinase; 2.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 2.

KW ATP-binding; Transferase.

SW SEQUENCE 794 AA; 89743 MW; 8595E1971337D9C CRC64;

Query Match 1.9%; Score 8; DB 5; Length 794;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 GSGGFGDV 139
|||||||
DB 468 GSGGFGDV 475

RESULT 44

ID Q9VAX8 PRELIMINARY; PRT; 975 AA.

AC Q9VAX8; 2000 (TrEMBLrel. 13, Created: 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) CG4849 protein (D28793p).

GN CG4849.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY.

RE MEDLINE=20196006; PubMed=10711132;

RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scher S.E., Li P.W., Hinkley R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Vandal M.D., Zhan Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer V.G., Hampe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bertram B.P., Bhattacharya D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Dwyer A., Dew I., Dietz S.M., Dodson K., Dou P.L., Downes M., Dugan-Roe S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Friera S., Fleischmann W., Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Hartie N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao X., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195(2000).

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarini H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S., Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celisner S.

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AE003763; AAF56769.1; --

DR EMBL: AY089551; AAL90289.1; --

DR FlyBase: FBgn0039566; CG4849.

DR InterPro: IPR000640; EFG-C.

DR InterPro: IPR005517; EFG-IV.

DR InterPro: IPR004161; EFTU_D2.

DR InterPro: IPR000795; EF_GTPbind.

DR InterPro: IPR005225; Small_GTP.

DR Pfam: PF00679; EFG_C; 1.

DR Pfam: PF03764; EFG-IV; 1.

DR Pfam: PF00009; GTP_EFTU; 1.

DR Pfam: PF03144; GTP_EFTU_D2; 1.

DR PRINTS: PR00315; ELONGATNFT.

DR TIGRFAMs: TIGR00231; small_GTP; 1.

KW GTP-binding; Protein biosynthesis.

SW SEQUENCE 975 AA; 110649 MW; 68A9072B3300E9CB CRC64;

Query Match 1.9%; Score 8; DB 5; Length 975;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 LLELRQD 223
|||||||
DB 961 LLELRQD 968

RESULT 45

Q962H8 PRELIMINARY; PRT; 1031 AA.

ID Q962H8

AC Q962H8; 2000 (TrEMBLrel. 19, Created: 01-DEC-2001 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 23, Last annotation update) DE Membrane skeleton protein IMC2.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE Membrane skeleton protein IMC2.

GN IMC2.

OS Toxoplasma gondii.

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

OX NCBI_TaxID=5911;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RH;

RE MEDLINE=21313687; PubMed=11420112;

RX Mann T., Beckers C.; "Characterization of the subpellicular network, a filamentous membrane

IT skeletal component in the parasite Toxoplasma gondii.";
Mol. Biochem. Parasitol. 115:257-268(2001).
[2]
RC SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Beckers C.J., Mann T.M.;
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032682; AAK39356.2; -;
DR InterPro; IPR004843; M-ppesrase.
DR Pfam; PF00149; Metallophos; 1.
SQ SEQUENCE 1031 AA; 117427 MW; 9EAB3A0E148BE4F4 CRC64;

Query Match 1.9%; Score 8; DB 5; Length 1031;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 RAGSGRR 52

|||||

Db 777 RAGSGRR 784

RESULT 46

Q8L899 PRELIMINARY; PRT; 1207 AA.

AC Q8L899;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Systemin receptor SR160.

OS Lycopersicon peruvianum (Peruvian tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamids; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4082;

[1]

SEQUENCE FROM N.A.

MEDLINE=22103620; PubMed=12060717;

Scheer J.M., Ryan C.A. Jr.;

"From the Cover: The systemin receptor SR160 from Lycopersicon

peruvianum is a member of the LRR receptor kinase family.";

Proc. Natl. Acad. Sci. U.S.A. 99:9585-9590(2002).

EMBL; AY112661; AAM48285.1; -;

InterPro; IPR001611; LRR.

InterPro; IPR007090; LRR_plant.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR002290; Ser_thr_kinase.

InterPro; IPR001245; Tyr_kinase.

Pfam; PF00069; pkinase; 1.

PRINTS; PS00502; LRR_PS; 5.

PRINTS; PS00019; LEURICHRPT.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKc; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00502; LRR_PS; 5.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Receptor; Transferase.

SEQUENCE 1207 AA; 131963 MW; 1422D1DFDA458073 CRC64;

Query Match

Best Local Similarity 1.9%; Score 8; DB 1; Length 1207;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGDV 139

|||||

Db 895 GSGGFGDV 902

RESULT 47

Q8GUQ5

ID Q8GUQ5

AC Q8GUQ5;

PRELIMINARY; PRT; 1207 AA.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE BRIL protein.
GN CURL3.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12468734;
RA Montoya T., Nomura T., Farrar K., Kaneta T., Yokota T., Bishop G.J.;
"Cloning the Tomato Cur3 Gene Highlights the Putative Dual Role of
the Leucine-Rich Repeat Receptor Kinase tBR11/SRI60 in Plant Steroid
Hormone and Peptide Hormone Signaling.";
RT Plant Cell 14:3163-3176(2002).
RL EMBL; AY179606; AAN85409.1; -;
SQ SEQUENCE 1207 AA; 131956 MW; 6C370BA048060B7F CRC64;

Query Match 1.9%; Score 8; DB 10; Length 1207;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGDV 139

|||||

Db 895 GSGGFGDV 902

RESULT 48

Q9EXM1

ID Q9EXM1

AC Q9EXM1;

PRELIMINARY; PRT; 91 AA.

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Chloroplast-type ferredoxin.

GN ALND.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

[1]

RP SEQUENCE FROM N.A.

RC TRANSPOSON=Tn5-Mob;

RX MEDLINE=98276889; PubMed=9614705;

RA Murakami S., Nakanishi Y., Kodama N., Takenaka S., Shinke R., Aoki K.;

"Purification, characterization, and gene analysis of catechol 2,3-

dioxygenase from the aniline-assimilating Pseudomonas species AW-2.";

RL Biosci. Biotechnol. Biochem. 62:747-752(1998).

DR EMBL; AB004065; BAB18932.1; -;

DR InterPro; IPR006058; 2Fe2S_ferredoxin.

DR InterPro; IPR001041; Ferredoxin.

DR Pfam; PF00111; fer2; 1.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

KW Iron; Iron-sulfur.

SEQUENCE 91 AA; 9529 MW; 8CF548719F903C5B CRC64;

Query Match

Best Local Similarity 1.7%; Score 7; DB 2; Length 91;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 AGKLSKP 101

|||||

Db 67 AGKLSKP 73

RESULT 49

Q8YLM1

ID Q8YLM1

AC Q8YLM1;

PRELIMINARY; PRT; 98 AA.

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

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JT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
JE HicA protein.
JE ASL5277.
JE
JE Anabaena sp. (strain PCC 7120).
JC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
JC NCBI_TaxID=103690;
JC [1]
JC SEQUENCE FROM N.A.
JC MEDLINE=21595285; PubMed=11759840;
JC Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
JC Watanabe A., Iriiguchi M., Iehikawa A., Kawashima K., Kimura T.,
JC Kishida Y., Kohara M., Matsumoto M., Matsuura A., Muraki A.,
JC Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
JC Yasuda M., Tabata S.;
JC "Complete genomic sequence of the filamentous nitrogen-fixing
JC cyanobacterium Anabaena sp. strain PCC 7120."
JC DNA Res. 8:205-213(2001).
JC EMBL; AP003599; BAB76976.1; ..
JC Complete proteome.
JC SEQUENCE 98 AA; 10947 MW; 7C1417F81813D7B9 CRC64;
JC
JC Query Match 1.7%; Score 7; DB 16; Length 98;
JC Best Local Similarity 100.0%; Pred. No. 86;
JC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JC
JC QY 366 TLDDIFE 372
JC |||||
JC Db 10 TLDDIFE 16
JC
JC RESULT 50
JC Q924C6 PRELIMINARY; PRT; 111 AA.
JC ID Q924C6 PRELIMINARY; PRT; 111 AA.
JC AC Q924C6;
JC DT 01-MAY-1999 (TEMBLrel. 10, Created)
JC DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
JC DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
JC DE YgfA protein (YdhA protein).
JC GN YGFA OR YDHA..
JC OS Salmonella typhimurium, and
JC OS Shigella sonnei.
JC OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
JC OC Enterobacteriaceae; Salmonella.
JC OX NCBI_TaxID=602, 624;
JC [1]
JC RN SEQUENCE FROM N.A.
JC RC SPECIES=S.typhimurium; PLASMID=R64;
JC RA Sampa G., Komano T., Sasaki T., Tachibana K., Furuya N., Saito Y.,
JC Suzuki T., Mizobuchi K.;
JC RT "Organization and diversification of plasmid genomes: complete
JC nucleotide sequence of R64 genome."
JC RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
JC [2]
JC RN SEQUENCE FROM N.A.
JC RC SPECIES=S.typhimurium; PLASMID=R64;
JC RA MEDLINE=87146423; PubMed=3029698;
JC RA Komano T., Kubo A., Nisioka T.;
JC RT "Shufflon: multi-inversion of four contiguous DNA segments of plasmid
JC R64 creates seven different open reading frames."
JC RT Nucleic Acids Res. 15:1165-1172(1987).
JC [3]
JC RN SEQUENCE FROM N.A.
JC RC SPECIES=S.typhimurium; PLASMID=R64;
JC RA MEDLINE=89127142; PubMed=3065610;
JC RA Kubo A., Kusukawa A., Komano T.;
JC RT "Nucleotide sequence of the rci gene encoding shufflon-specific DNA
JC recombinase in the IncII plasmid R64: homology to the site-specific
JC Mol. Gen. Genet. 213:30-35(1988).
JC [4]
JC RN SEQUENCE FROM N.A.
JC RC SPECIES=S.typhimurium; PLASMID=R64;
JC
RC SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=88314948; PubMed=3045094;
RA Komano T., Toyoshima A., Morita K., Nisioka T.;
RT "Cloning and nucleotide sequence of the orit region of the IncII
RT plasmid R64."
RL J. Bacteriol. 170:4385-4387(1988).
RN [5]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=91177811; PubMed=1848841;
RA Furuya N., Nisioka T., Komano T.;
RT "Nucleotide sequence and functions of the orit operon in IncII plasmid
RT R64."
RL J. Bacteriol. 173:2231-2237(1991).
RN [6]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=92011438; PubMed=1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at orit of IncII plasmid R64: global
RT similarity of orit structures of IncII and IncP plasmids."
RL J. Bacteriol. 173:6612-6617(1991).
RN [7]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=93352408; PubMed=8349545;
RA Kim S.R., Funayama N., Komano T.;
RT "Nucleotide sequence and characterization of the traABCD region of
RT IncII plasmid R64."
RL J. Bacteriol. 175:5035-5042(1993).
RN [8]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=95083745; PubMed=7991676;
RA Furuya N., Komano T.;
RT "Surface exclusion gene of IncII plasmid R64: nucleotide sequence and
RT analysis of deletion mutants."
RL Plasmid 32:80-84(1994).
RN [9]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=96198148; PubMed=8626273;
RA Furuya N., Komano T.;
RT "Nucleotide sequence and characterization of the pnd gene for plasmid maintenance
RT within the transfer region."
RL J. Bacteriol. 178:1491-1497(1996).
RN [10]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=97428559; PubMed=9281491;
RA Narihara K., Rahman E., Furuya N., Komano T.;
RT "Requirement of a limited segment of the sog gene for plasmid R64
RT conjugation."
RL Plasmid 38:1-11(1997).
RN [11]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=97315231; PubMed=9171405;
RA Kim S.R., Komano T.;
RT "The plasmid R64 thin pilus identified as a type IV pilus."
RL J. Bacteriol. 179:3594-3603(1997).
RN [12]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;
RX MEDLINE=98053841; PubMed=939369;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 orit region: requirement for precise
RT location of the Nika-binding sequence."
RL J. Bacteriol. 179:7291-7297(1997).
RN [13]
RN SEQUENCE FROM N.A.
RN SPECIES=S.typhimurium; PLASMID=R64;

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MEDLINE=98268996; PubMed=9603870;
Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,
Ogawa T., Komano T.;
" Purification and characterization of thin pili of IncII plasmids
Colib-P9 and R64: formation of PiliV-specific cell aggregates by type
IV pili.";
J. Bacteriol. 180:2842-2848(1998).
[14]
SEQUENCE FROM N.A.
SPECIES=S.typhimurium; PLASMID=R64;
MEDLINE=20233621; PubMed=10760136;
Komano T., Yoshida T., Nakahara K., Furuya N.;
"The transfer region of IncII plasmid R64: similarities between R64
tra genes and Legionella icm/dot genes.";
Mol. Microbiol. 35:1348-1359(2000).
[15]
SEQUENCE FROM N.A.
SPECIES=S.sonnei; STRAIN=P9; PLASMID=Colib-P9;
Sampei G., Mizobuchi K.;
"Organization and diversification of plasmid genomes: complete
nucleotide sequence of the Colib-P9 genome.";
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
EMBL; AP005147; BAB91640.1; -.
EMBL; AB021078; BAA75137.1; -.
Plasmid.
SEQUENCE 111 AA; 12199 MW; 59EA33B7238397E1 CRC64;

Query Match      1.74; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred.No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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db 22 LRRRFSS 28

Search completed: October 20, 2003, 12:27:08
Job time : 105 secs

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GenCore version 5.1
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ord size : 0

total number of hits satisfying chosen parameters 1107863

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 3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
 5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
 6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
 7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
 8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
 9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
 13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
 15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
 16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
 17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
 18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
 19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
 24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score c, the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	416	100.0	416	19	AAW39209	Human ICE LAP-6 po
2	416	100.0	416	22	AAE00606	Human caspase-9, a
3	219	52.6	416	20	AA21723	Amino acid sequenc
4	219	52.6	416	23	ABJ01224	Human caspase-9 SE
5	202	48.6	203	19	AAW39208	Human ICE LAP-6 am
6	195	46.9	416	22	AAE08938	Mammalian ced-3 ho
7	195	46.9	416	22	AAE08938	Amino acid sequenc
8	195	46.9	416	22	AAE08938	Amino acid sequenc
9	195	46.9	416	22	AAU08315	Human aspartate-ep

10	195	46.9	416	24	ABB82738	Human caspase-9 po
11	127	30.5	266	22	AAE00620	Human caspase-9.
12	93	22.4	93	23	ABJ04760	Caspase-9 protein
13	42	10.1	42	24	ABP71130	Mch6 CARD protein
14	19	4.6	19	24	ABP71130	Mch6 protein CARD
15	15	3.6	15	20	AAE08955	Conserved peptide
16	15	3.6	15	20	AAE08955	Mammalian ced-3 ho
17	15	3.6	15	23	ABJ01243	Human caspase cons
18	15	3.6	15	24	ABE08939	Human caspase-9-pl
19	15	3.6	15	24	ABE08939	Mammalian ced-3 ho
20	14	3.4	14	22	AAE08939	Human caspase-9
21	12	2.9	12	22	AAU08321	Human Mch6 conserv
22	11	2.6	11	20	AAE08938	Aspartate-specific
23	11	2.6	11	20	AAE08938	Drosophila melanog
24	11	2.6	11	20	AAE08938	Mch6 protein CARD
25	10	2.4	10	24	ABP71122	Human bone marrow
26	10	2.4	10	24	ABP71122	Human bone marrow
27	10	2.4	10	24	ABP71122	Human bone marrow
28	10	2.4	10	24	ABP71122	Human bone marrow
29	10	2.4	10	24	ABP71122	Human bone marrow
30	10	2.4	10	24	ABP71122	Human bone marrow
31	10	2.4	10	24	ABP71122	Human bone marrow
32	10	2.4	10	24	ABP71122	Human bone marrow
33	10	2.4	10	24	ABP71122	Human bone marrow
34	10	2.4	10	24	ABP71122	Human bone marrow
35	10	2.4	10	24	ABP71122	Human bone marrow
36	10	2.4	10	24	ABP71122	Human bone marrow
37	10	2.4	10	24	ABP71122	Human bone marrow
38	10	2.4	10	24	ABP71122	Human bone marrow
39	10	2.4	10	24	ABP71122	Human bone marrow
40	10	2.4	10	24	ABP71122	Human bone marrow
41	10	2.4	10	24	ABP71122	Human bone marrow
42	10	2.4	10	24	ABP71122	Human bone marrow
43	10	2.4	10	24	ABP71122	Human bone marrow
44	10	2.4	10	24	ABP71122	Human bone marrow
45	10	2.4	10	24	ABP71122	Human bone marrow
46	10	2.4	10	24	ABP71122	Human bone marrow
47	10	2.4	10	24	ABP71122	Human bone marrow
48	10	2.4	10	24	ABP71122	Human bone marrow
49	9	2.2	9	20	AAE08952	Conserved peptide
50	9	2.2	9	20	AAE08952	Mammalian ced-3 ho
51	9	2.2	9	20	AAE08952	Human Mch6 conserv
52	9	2.2	9	20	AAE08952	Human caspase cons
53	9	2.2	9	20	AAE08952	Mouse CFLIP-L prot
54	9	2.2	9	20	AAE08952	FLICE-like inhibi
55	9	2.2	9	20	AAE08952	Mouse FLIP-c prote
56	9	2.2	9	20	AAE08952	Murine FLIP protei
57	9	2.2	9	20	AAE08952	Mouse FLIP-c prote
58	9	2.2	9	20	AAE08952	Amino acid sequenc
59	9	2.2	9	20	AAE08952	Herbicidally activ
60	9	2.2	9	20	AAE08952	Arabidopsis sterol
61	9	2.2	9	20	AAE08952	Amino acid sequenc
62	9	2.2	9	20	AAE08952	Brassinosteroid re
63	9	2.2	9	20	AAE08952	Propionibacterium
64	8	1.9	8	22	AAU55290	M. tuberculosis an
65	8	1.9	8	22	AAU55290	Drosophila melanog
66	8	1.9	8	22	AAU55290	Chlamydia pneumoni
67	8	1.9	8	22	AAU55290	Human secreted pro
68	7	1.7	7	50	ABP33198	Human ORF2171 prot
69	7	1.7	7	50	ABP33198	Human polypeptide
70	7	1.7	7	50	ABP33198	Propionibacterium
71	7	1.7	7	50	ABP33198	Human ORF4271 prot
72	7	1.7	7	50	ABP33198	Human ORF4271 prot
73	7	1.7	7	50	ABP33198	Peptide #10881 enc
74	7	1.7	7	50	ABP33198	Human ORFX protein
75	7	1.7	7	50	ABP33198	Peptide #10881 enc

ALIGNMENTS

RESULT 1
 AAW39209

AAW39209 standard; peptide; 416 AA.
 AAW39209;
 18-MAY-1998 (first entry)
 Human ICE LAP-6 polypeptide.
 ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
 viral infection; tumour; inflammation; osteoporosis; AIDS; human;
 Alzheimer's disease.
 Homo sapiens.
 EP808904-A2.
 26-NOV-1997.
 19-MAY-1997; 97EP 0303397.
 05-JUN-1996; 96US-0018961.
 20-MAY-1996; 96US-0017949.
 23-MAY-1996; 96US-0020344.
 (HUMA-) HUMAN GENOME SCI INC.
 (SMIK-) SMITHKLINE BEECHAM CORP.
 (UNMI-) UNIV MICHIGAN.
 Dixit VM, He W, Kikly KK, Ruben SM;
 WPI: 1998-001790/01.
 N-PSDB; AAV09401.
 DNA encoding interleukin-1 beta converting enzyme apoptosis
 protease-6 - useful to develop products to treat, e.g. viral
 infection, tumour, Alzheimer's disease, inflammation, osteoporosis
 and AIDS
 Claim 4; Fig 1; 44pp; English.
 This is a human interleukin-1 beta converting enzyme apoptosis protease-6
 (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the
 polypeptide can be used to induce apoptosis, e.g. as an antiviral or
 antitumour agent, control embryonic development and tissue homeostasis
 and the roles of such factors in dysfunction and disease. Antagonists
 which inhibit the activity of the ICE LAP-6 polypeptide can be used to
 treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic
 shock, sepsis, stroke, chronic, acute or central nervous system
 inflammation, osteoporosis, ischaemia reperfusion injury, cell death
 associated with cardiovascular disease, polycystic kidney disease,
 apoptosis of endothelial cells in cardiovascular disease, degenerative
 liver disease, multiple sclerosis, cerebellar degeneration, ischaemic
 injury, myocardial infarction, acquired immunodeficiency syndrome (AIDS),
 myelodysplastic syndrome, aplastic anaemia, male pattern baldness and
 head injury damage. They can also be used for detection and diagnosis.

Sequence 416 AA;

Query Match 100.0%; Score 416; DB 19; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDEADRLRLRRLRLVEELQVDQLWDLVLLSRELPHMIEDIQAGSGRRDQARQLII 60
 1 MDEADRLRLRRLRLVEELQVDQLWDLVLLSRELPHMIEDIQAGSGRRDQARQLII 60
 61 DLETRGQALPLFISCLDTGDMMLASFLRNRQAGKLSKPTLENLTVPVLRPIRPEV 120
 61 DLETRGQALPLFISCLDTGDMMLASFLRNRQAGKLSKPTLENLTVPVLRPIRPEV 120
 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPEPCGCHLIINNPNFCRESGLRTR 180
 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPEPCGCHLIINNPNFCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSJHFMVEVKGDLTAKQWVLALELARDHGLDCCVVVILSHGCQ 240
 DB 181 TGSNIDCEKLRFRFSSJHFMVEVKGDLTAKQWVLALELARDHGLDCCVVVILSHGCQ 240
 QY 241 ASHLQPPGAVYGTDCGCVSVSEKIVNIFNGTSCPSLGGKPKLFFIACGGEQKDHGFEVAS 300
 DB 241 ASHLQPPGAVYGTDCGCVSVSEKIVNIFNGTSCPSLGGKPKLFFIACGGEQKDHGFEVAS 300
 QY 301 TSPEDSPGSPNEPDATPFOEGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
 DB 301 TSPEDSPGSPNEPDATPFOEGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMGCFNLRKKLFFKTS 416
 DB 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMGCFNLRKKLFFKTS 416
 RESULT 2
 AAE00606
 ID AAE00606 standard; Protein; 416 AA.
 XX
 AC AAE00606;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Human caspase-9, alternative version.
 XX
 KW Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 28 /note= "Encoded by GGC; Ala is present in the sequence
 FT shown in page 105-107 (AAE00620)"
 FT Misc-difference 96 /note= "Encoded by GCA; Ala is present in the sequence
 FT shown in page 105-107 (AAE00620)"
 FT Misc-difference 139..290 /note= "Encoded by GTCGAG; Amino acid residues from
 FT position 140 to 289 present in this sequence are not
 FT found in the sequence shown in page 105-107 (AAE00620)"
 FT Cleavage-site 315..316 /label= Proteolytic_cleavage_site
 FT Cleavage-site 330..331 /label= Proteolytic_cleavage_site
 FT WO200129232-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 19-OCT-2000; 2000WO-US28941.
 XX
 PR 20-OCT-1999; 99US-0160559.
 PR 14-AUG-2000; 2000US-0225564.
 XX
 PA (SCIO-) SCIOS INC.
 XX
 PI Cordell B, Li Y;
 XX
 DR WPI: 2001-290920/30.
 DR N-PSDB; AAD03916.
 XX
 PT Novel fusion polypeptide comprising first and second caspase subunit
 PT separated by cleavage site not associated in nature with caspase
 PT subunit, useful for cloning gene encoding enzymes involved in
 PT proteolytic cleavage
 XX
 PS Claim 4; Fig 18; 116pp; English.
 XX

C The present sequence is an alternative version of human Caspase-9 also
 C known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases
 C are a family of cysteine proteases, that participate in the initiation
 C and execution of apoptosis. Caspases exist as pro-enzymes, activated by
 C cleavage into a large and small subunit, occurring after specific
 C aspartic acid residues within the pro-enzyme sequence.
 C The present invention relates to a method for functional cloning of genes
 C encoding proteins or enzymes involved in proteolytic cleavage. The
 C invention is based on the use of caspase expression cassettes comprising
 C the coding sequence of a proteolytic cleavage site flanked by sequences
 C encoding two caspase subunits. A fusion polypeptide comprising a first
 C and a second caspase subunit, separated by a cleavage site not associated
 C in nature, is useful for cloning gene encoding enzymes involved in
 C proteolytic cleavage. An expression cassette containing fusion
 C polypeptide is used to identify a mutant cell line deficient in an
 C enzyme of interest and is also useful for diagnosis and suppression of
 C proliferation or metastases of a tumour cell characterised by
 C overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
 C selectively expressed in the tumour cells). DNA encoding fusion
 C polypeptide is used in gene therapy.
 C Note: This sequence SEQ ID NO.18 is stated as being the same as that
 C shown in page 105-107 (See AAE00620) in the specification. However these
 C sequences differ at several positions.

XX Sequence 416 AA;

Query Match 100.0%; Score 416; DB 22; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MDEADRLRLRLRLVEELQVDLQDVLRLPHMIEDIQAGSGSRDQARQLII 60
 1 MDEADRLRLRLRLVEELQVDLQDVLRLPHMIEDIQAGSGSRDQARQLII 60
 61 DLETRGSQLPLFISCLDTGQDMLASFLTRNRQAGLSKPTLENLTPVLRPEIRKEV 120
 61 DLETRGSQLPLFISCLDTGQDMLASFLTRNRQAGLSKPTLENLTPVLRPEIRKEV 120
 121 LRPETPRPVDIGSGGFGDVGALSLRGADLALYILSMPCGCHLIINNVEFCRESGLRTR 180
 121 LRPETPRPVDIGSGGFGDVGALSLRGADLALYILSMPCGCHLIINNVEFCRESGLRTR 180
 181 TGSNIDCEKLRRLRRFSLHFMVEVKGDLTAKKMWLALLELRQDHGALDCCVVVILSHGCG 240
 181 TGSNIDCEKLRRLRRFSLHFMVEVKGDLTAKKMWLALLELRQDHGALDCCVVVILSHGCG 240
 241 ASHLQFPCAVVTGDCGCVSVKEIVNI FNGTSCPSLGGKPKLFFIOACGGEQKHGFVEAS 300
 241 ASHLQFPCAVVTGDCGCVSVKEIVNI FNGTSCPSLGGKPKLFFIOACGGEQKHGFVEAS 300
 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISSLTPSDIFVSYSTFPFGVSWRDPKSG 360
 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISSLTPSDIFVSYSTFPFGVSWRDPKSG 360
 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMPCCFNFLRKLFFKTS 416
 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMPCCFNFLRKLFFKTS 416

RESULT 3

AA21723
 ID AAY21723 standard; Protein; 416 AA.

XX AAY21723;

XX 10-SEP-1999 (first entry)

XX Amino acid sequence of caspase-9 (ICE-LAP6).

XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 XX autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 XX tumour cell; myocardial infarction; human.

OS Homo sapiens.
 XX WO9935277-A2.
 XX 15-JUL-1999.
 XX 11-JAN-1999; 99WO-US00632.
 XX 09-JAN-1998; 98US-0070987.
 XX (UJVE-) UNIV JEFFERSON THOMAS.
 XX Alnemri ES;
 XX WPI; 1999-419353/35.
 XX N-PSDB; AAX81225.
 XX New isolated nucleic acid molecule encoding a rev-caspase - used
 XX for screening and identifying inhibitors or enhancers for treating
 XX cancer or autoimmune disease
 XX Disclosure; Fig 19A-B; 74pp; English.
 XX The invention relates to nucleic acid molecules encoding rev-caspases.
 XX Rev-caspases are cysteine proteases that specifically cleave proteins
 XX after Asp residues and is expressed as a zymogen, in which the small
 XX subunit is N-terminal to a large subunit. A gene delivery vehicle
 XX comprising a rev-caspase coding sequence is useful for the treatment of
 XX cancer, where the gene delivery vehicle is internalised by tumour cells.
 XX The gene delivery vehicle can also be used to treat autoimmune diseases.
 XX Cells transfected with a rev-caspase expressing vector can be used in
 XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
 XX In vitro translated rev-caspase can be used to identify an inhibitor or
 XX enhancer of caspase processing activity. Caspase inhibitors are useful
 XX for treating neurodegenerative diseases as well as for inhibiting
 XX apoptosis in the heart following myocardial infarction. Sequences
 XX AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
 XX gene products (AAY21715-Y21724).
 XX Sequence 416 AA;

Query Match 52.6%; Score 219; DB 20; Length 416;
 Best Local Similarity 100.0%; Pred. No. 6.6e-208;

Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 HFWEVKGDLTAKKMWLALLELRQDHGALDCCVVVILSHGQASHLQPPGAVGTDCGP 257
 DB 198 HFWEVKGDLTAKKMWLALLELRQDHGALDCCVVVILSHGQASHLQPPGAV GTDCGP 257
 QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKHGFVEASTSPDESFGSNPEPDAT 317
 DB 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKHGFVEASTSPDESFGSNPEPDAT 317
 QY 318 PFQEGRLTFDQDLAISSLTPSD FVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHS 377
 DB 318 PFQEGRLTFDQDLAISSLTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAHS 377
 QY 378 EDLSLLLRVANAVSVKGIYKOMPCCFNFLRKLFFKTS 416
 DB 378 EDLSLLLRVANAVSVKGIYKOMPCCFNFLRKLFFKTS 416

RESULT 4

ABJ01224
 ID ABJ01224 standard; Protein; 416 AA.

XX AC ABJ01224;

XX 18-SEP-2002 (first entry)

XX Human caspase-9 SEQ ID NO: 30.

XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis;

KW cancer; autoimmune disease; cytostatic; immunosuppressive.
XX Homo sapiens.
OS
XX US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-0561756.
XX
XX 09-JAN-1998; 98US-070897P.
XX
XX 08-JAN-1999; 99US-0227721.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-451275/48.
XX
XX N-PSDB; ABT03972.
XX
XX New rev-caspases engineered to contain the small subunit fused in frame
XX N-terminal to the large subunit, which is in reverse order to the wild
XX type caspases, are useful to treat cancer and autoimmune diseases.
XX
XX Disclosure; Fig 19; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
XX can be used in the gene therapy of cancer and autoimmune diseases. The
XX present sequence is a protein described in the exemplification of the
XX invention.
XX
XX Sequence 416 AA;
SQ
Query Match 52.6%; Score 219; DB 23; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.6e-208;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 HFMEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCOASHLOFPGAVYGTGDCP 257
DB 198 HFMEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCOASHLOFPGAVYGTGDCP 257
QY 258 VSVEKIVNIFNGTSCPSLGGCKPKLFFIQACGGEQDGHGFEVASTSPEDSPGSNPEPDAT 317
DB 258 VSVEKIVNIFNGTSCPSLGGCKPKLFFIQACGGEQDGHGFEVASTSPEDSPGSNPEPDAT 317
QY 318 PQEGLRTFDQLDAISLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQMAHS 377
DB 318 PQEGLRTFDQLDAISLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQMAHS 377
QY 378 EDLQSLLRVANAVSVKGIYKMPGCCFNFLRKKLFFKTS 416
DB 378 EDLQSLLRVANAVSVKGIYKMPGCCFNFLRKKLFFKTS 416
RESULT 5
AAW39208
ID AAW39208 standard; peptide; 203 AA.
XX
XX AAW39208;
XX
XX 18-MAY-1998 (first entry)
XX
XX Human ICE LAP-6 amino acid sequence variant.
XX
XX ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
XX viral infection; tumour; inflammation; osteoporosis; AIDS; human;
XX Alzheimer's disease; variant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 203
FT

FT
XX EP808904-A2.
XX
XX 26-NOV-1997.
XX
XX 19-MAY-1997; 97EP-0303397.
XX
XX 05-JUN-1996; 96US-0018961.
XX
XX 20-MAY-1996; 96US-0017949.
XX
XX 23-MAY-1996; 96US-0020344.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (UNMI) UNIV MICHIGAN.
XX
XX Dixit VM, He W, Kikly KK, Ruben SM;
XX
XX WPI; 1998-001790/01.
XX N-PSDB; AAV09402.
XX
XX DNA encoding interleukin-1 beta converting enzyme apoptosis
XX protease-6 - useful to develop products to treat, e.g. viral
XX infection, tumour, Alzheimer's disease, inflammation, osteoporosis
XX and AIDS
XX
XX Disclosure; Fig 5; 44pp English.
XX
XX This is an amino acid sequence variant of human interleukin-1 beta
XX converting enzyme apoptosis protease-6 (ICE LAP-6) polypeptide. The ICE
XX LAP-6 polypeptide and agonists to the polypeptide can be used to induce
XX apoptosis, e.g. as an antiviral or antitumour agent, control embryonic
XX development and tissue homeostasis and the roles of such factors in
XX dysfunction and disease. Antagonists which inhibit the activity of the
XX ICE LAP-6 polypeptide can be used to treat, Alzheimer's or Parkinson's
XX disease, rheumatoid arthritis, septic shock, sepsis, stroke, chronic,
XX acute or central nervous system inflammation, osteoporosis, ischaemia
XX reperfusion injury, cell death associated with cardiovascular disease,
XX polycystic kidney disease, apoptosis of endothelial cells in
XX cardiovascular disease, degenerative liver disease, multiple sclerosis,
XX cerebellar degeneration, ischaemic injury, myocardial infarction,
XX acquired immunodeficiency syndrome (AIDS), myelodysplastic syndrome,
XX aplastic anaemia, male pattern baldness and head injury damage. They can
XX also be used for detection and diagnosis.
XX
XX Sequence 203 AA;
SQ
Query Match 48.6%; Score 202; DB 19; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.4e-191;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 212 MVLALLELARQDHGALDCCVVVILSHGCOASHLOFPGAVYGTGDCPVSVEKIVNIFNGTS 271
DB 1 MVLALLELARQDHGALDCCVVVILSHGCOASHLOFPGAVYGTGDCPVSVEKIVNIFNGTS 60
QY 272 CPSLGGCKPKLFFIQACGGEQDGHGFEVASTSPEDSPGSNPEPDATPFGGLRTFDQLDA 331
DB 61 CPSLGGCKPKLFFIQACGGEQDGHGFEVASTSPEDSPGSNPEPDATPFGGLRTFDQLDA 120
QY 332 ISSLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQMAHSEDQLSLLRVANAV 391
DB 121 ISSLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQMAHSEDQLSLLRVANAV 180
QY 392 SVKGIYKMPGCCFNFLRKKLFF 413
DB 181 SVKGIYKMPGCCFNFLRKKLFF 202
RESULT 6
AAE08938
ID AAE08938 standard; Protein; 416 AA.
XX
XX AAE08938;
AC

```
XX
DT 15-NOV-2001 (first entry)
XX
DE Mammalian ced-3 homologue 6 (Mch6) .
XX
XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
XX aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
XX autoimmune disease; cerebellar degeneration; Alzheimer's disease;
XX cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
XX viral infection; cell death-mediated disease; neuroprotective.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
XX Active-site 285..290
XX /note= "Active site pentapeptide"
XX Cleavage-site 315..316
XX Cleavage-site 330..331
XX
XX USG271361-B1.
XX
XX 07-AUG-2001.
XX
XX 25-FEB-1999; 99US-0257218.
XX
XX 29-MAY-1997; 97US-0865579.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandes-alnemri T, Litwack G;
XX WPI; 2001-528686/58.
XX N-PSDB; AAD15656.
XX
XX New apoptotic genes and their apoptotic protease products, useful for
XX modulating apoptosis for the therapeutic treatment of human diseases,
XX e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
XX disease -
XX
XX Claim 2; Fig 1; 36pp; English.
XX
XX The invention relates to an isolated gene encoding apoptotic protease,
XX mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the
XX aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and
XX protein sequences are useful for modulating apoptosis for the
XX therapeutic treatment of human diseases. Mch6 sequences are useful
XX for upregulating apoptosis (e.g. for treating cancers, autoimmune
XX disease or viral infections) or downregulating apoptosis (e.g. for
XX treating Alzheimer's disease, Parkinson's disease or cerebellar
XX degeneration). The Mch6 sequence is useful for diagnosing, treating
XX or reducing the severity of cell death-mediated diseases, as well as
XX other diseases mediated by either increased or decreased programmed
XX cell death. The present amino acid sequence is Mch6.
XX
XX Sequence 416 AA;
XX
XX Query Match 46.9%; Score 195; DB 22; Length 416;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-184;
XX Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 222 QDHGALDCVVVILSHGQASHLOPPGAVYGTDCPVSVKEIVNIFNGTSCPSLGKPKL 281
XX |||||||
XX 222 QDHGALDCVVVILSHGQASHLOPPGAVYGTDCPVSVKEIVNIFNGTSCPSLGKPKL 281
XX |||||||
XX 282 FFIQACGGEQKHGFEVASTPEDESPGNSPEPATPFQEGRLTFDQLDAISLPTPSDI 341
XX |||||||
XX 282 FFIQACGGEQKHGFEVASTPEDESPGNSPEPATPFQEGRLTFDQLDAISLPTPSDI 341
XX |||||||
XX 342 FVSYSTPFGFVSWRDPKSGSVYVETLDDIFEQWAHSFLQSLLRVANAVSVKGYKOMP 401
XX |||||||
XX 342 FVSYSTPFGFVSWRDPKSGSVYVETLDDIFEQWAHSFLQSLLRVANAVSVKGYKOMP 401
XX |||||||
XX 402 GCFNFLRKKLFFKTS 416
XX
```

```
Db 402 GCFNFLRKKLFFKTS 416
|||||
RESULT 7
AAG67375
ID AAG67375 standard; Protein; 416 AA.
XX
AC AAG67375;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of human Mch6 polypeptide.
XX
XX Mch6; ced-3 homologue; ICE; interleukin-1-beta converting enzyme;
XX aspartate-specific cysteine protease; ASCP; apoptotic cell death;
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX retinitis pigmentosa; cerebellar degeneration; myelodysplastic syndrome;
XX aplastic anemia; ischemic injury; myocardial infarction; stroke; cancer;
XX reperfusion injury; autoimmune disease; systemic lupus erythematosus;
XX immune-mediated glomerulonephritis; viral infection; cell death.
XX
XX Homo sapiens.
XX
XX OS US6274318-B1.
XX
XX PN 14-AUG-2001.
XX
XX PD 13-MAY-1999; 99US-0311760.
XX
XX PF 29-MAY-1997; 97US-0865579.
XX
XX PR (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX PA Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX PI WPI; 2001-540372/60.
XX
XX DR N-PSDB; AAH77927.
XX
XX PT Identifying mammalian homologue ced-3 homolog (Mch6) activity modulators,
XX useful for treating lymphomas, carcinomas and hormone dependent tumours,
XX PT Alzheimer's disease, Parkinson's disease, comprises using Mch6
XX polypeptide -
XX
XX Example 1; Fig 1a-c; 36pp; English.
XX
XX The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
XX homologue, and is a member of the ICE (interleukin-1-beta converting
XX enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
XX specification describes a method for identifying mammalian Mch6 activity
XX modulators (inhibitors or enhancers). The compounds identified by the
XX method are useful as pharmaceuticals for treating or preventing diseases
XX characterized by increased apoptotic cell death such as Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
XX pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such
XX as aplastic anemia, ischemic injury including myocardial infarction,
XX stroke and reperfusion injury. The compounds are also useful for
XX treating diseases characterized by loss of apoptotic cell death such
XX as cancers, e.g. lymphomas, carcinomas and hormone dependent tumours
XX such as breast, prostate and ovarian cancer. Increased cell survival
XX or apoptosis inhibition also results in autoimmune diseases such as
XX systemic lupus erythematosus and immune-mediated glomerulonephritis as
XX well as viral infections such as herpes virus, pox virus and adenovirus
XX and the novel identified compounds are useful for treating these
XX conditions. The Mch6 inhibitors are used to treat or to reduce severity
XX of diseases characterized by increased programmed cell death.
XX
XX Sequence 416 AA;
XX
XX Query Match 46.9%; Score 195; DB 22; Length 416;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-184;
XX Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


homologue 6) an aspartate-specific cysteine protease and the MCH6 polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell death-mediated diseases (i.e. apoptotic) such as neurodegenerative diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury, myocardial infarction, stroke and reperfusion injury. The MCH6-encoding nucleic acids and polypeptides can also be used to diagnose or generate reagents to diagnose diseases mediated or characterised by programmed cell death. A purified recombinant MCH6 protein can be used to measure hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in a continuous fluorometric assay. The present sequence represents human MCH6.

```

Sequence 416 AA;
Query Match 46.9%; Score 195; DB 22; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.8e-184;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

222	QDHGALDCCVWILSHGCOASHLQFPCAVYGTGCGPVSVEKIWINIFNGTSCPSLGGKPKL	281
222	QDHGALDCCVWILSHGCOASHLQFPCAVYGTGCGPVSVEKIWINIFNGTSCPSLGGKPKL	281
222	QDHGALDCCVWILSHGCOASHLQFPCAVYGTGCGPVSVEKIWINIFNGTSCPSLGGKPKL	281
282	FFIQACGGQKOHGFEVASTSPEDSPGNSPEPDATPFQEGURTFDLODAISSLPTPSDI	341
282	FFIQACGGQKOHGFEVASTSPEDSPGNSPEPDATPFQEGURTFDLODAISSLPTPSDI	341
342	FVSYSTFPFGVSMRDPKSGSWYVETLDDIFEQWAHSEDIQSLLLRVANAVSVKGIYKOMP	401
342	FVSYSTFPFGVSMRDPKSGSWYVETLDDIFEQWAHSEDIQSLLLRVANAVSVKGIYKOMP	401
402	GCNFNLKRLKLFKTS	416
402	GCNFNLKRLKLFKTS	416

SULT 10
B82738
ABB82738 standard; Protein; 416 AA.

ABB82738;
07-MAR-2003 (first entry)
Human caspase-9 polypeptide.
Caspase-9; TUCAN; cancer; biomarker; cIAP2; Araf1; Bcl-2; Smac;
human.
Homo sapiens.
WO200290931-A2.
14-NOV-2002.
07-MAY-2002; 2002WO-US14487.
07-MAY-2001; 2001US-289223P.
12-FEB-2002; 2002US-356934P.
(BURN-) BURNHAM INST.

Reed JC;
WPI; 2003-111999/10.
Determining a prognosis for survival for a cancer patient, useful for determining if the patient is at risk for relapse, comprises measuring a level of TUCAN in a sample from the patient, and comparing it to a reference level -

Examples; Page 125-126; 153pp; English.

The invention relates to determining a prognosis for survival for a cancer patient. The method involves (a) measuring a level of a tumour up-regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic cell-containing sample from the cancer patient; and (b) comparing the level of TUCAN in the sample to a reference level of TUCAN, where a low level of TUCAN in the sample correlates with increased survival of the patient. Alternatively, the method involves measuring levels of TUCAN and one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or Smac in a neoplastic cell-containing sample from the cancer patient. The method is useful for determining if the patient is at risk for relapse, or for determining a proper course of treatment for a patient with cancer. The method is also useful for monitoring the effectiveness of a course of treatment for a patient with cancer, e.g. colon cancer, gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer, leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The present sequence represents a human caspase-9 polypeptide

Sequence 416 AA;

```
Query Match      46.9%; Score 195; DB 24; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.8e-184;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	222	QDHGALDCVVVILLSHGQASHLOFPGAVYGTGCPVSVKEKIVNIFNGTSCPSLGGKPKL	281
Db	222	QDHGALDCVVVILLSHGQASHLOFPGAVYGTGCPVSVKEKIVNIFNGTSCPSLGGKPKL	281
Qy	282	FFIOACGGEQKDHGFEVASTSPEDSPGSNPEPATPFQEGUPTFDQLDAISSLPTPSDI	341
Db	282	FFIOACGGEQKDHGFEVASTSPEDSPGSNPEPATPFQEGUPTFDQLDAISSLPTPSDI	341
Qy	342	FVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAKHSEDQLSLLRVANAVSVKGIYKQMP	401
Db	342	FVSYSTFPFGVSWRDPKSGSWYVETLDDIFEQWAKHSEDQLSLLRVANAVSVKGIYKQMP	401
Qy	402	GCNFRLRKKLFKNTS	416
Db	402	GCNFRLRKKLFKNTS	416

RESULT 11
AAE00620
ID AAE00620 standard; Protein; 266 AA.

AAE00620;
02-JUL-2001 (first entry)
Human caspase-9.
Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6; cysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy.
Homo sapiens.
Key Location/Qualifiers
Cleavage-site 165..166 /label= Proteolytic_cleavage_site
Cleavage-site 180..181 /label= Proteolytic_cleavage_site
WO200129232-A2.

XX	26-APR-2001.	
PD		
XX		
PF	19-OCT-2000; 2000WO-US28941.	
XX		
PR	20-OCT-1999; 99US-0160559.	
PR	14-AUG-2000; 2000US-0225564.	

PA (SCIO-) SCIOS INC.
 XX Cordell B, Li Y;
 PI WPI; 2001-290920/30.
 DR N-PSDB; AAD03916.
 XX
 XX Novel fusion polypeptide comprising first and second caspase subunit
 PT separated by cleavage site not associated in nature with caspase
 PT subunit, useful for cloning gene encoding enzymes involved in
 PT proteolytic cleavage
 XX
 XX Claim 4; Page 105-107; 116pp; English.
 PS
 XX The present amino acid sequence is human Caspase-9 also known as
 CC interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases are
 CC a family of cysteine proteases, that participate in the initiation and
 CC execution of apoptosis. Caspases exist as pro-enzymes, activated by
 CC cleavage into a large and small subunit, occurring after specific
 CC aspartic acid residues within the pro-enzyme sequence.
 CC The present invention relates to a method for functional cloning of genes
 CC encoding proteins or enzymes involved in proteolytic cleavage. The
 CC invention is based on the use of caspase expression cassettes comprising
 CC the coding sequence of a proteolytic cleavage site flanked by sequences
 CC encoding two caspase subunits. A fusion polypeptide comprising a first
 CC and a second caspase subunit, separated by a cleavage site not associated
 CC in nature, is useful for cloning gene encoding enzymes involved in
 CC proteolytic cleavage. An expression cassette containing fusion
 CC polypeptide is used to identify a mutant cell line deficient in an
 CC enzyme of interest and is also useful for diagnosis and suppression of
 CC proliferation or metastases of a tumour cell characterised by
 CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
 CC selectively expressed in the tumour cells). DNA encoding fusion
 CC polypeptide is used in gene therapy.
 CC Note: This sequence SEQ ID NO.18 is stated as being the same as that
 CC shown in Figure 18 (See AAE0606) in the specification. However these
 CC sequences differ at several positions.
 XX
 SQ Sequence 266 AA;
 Query Match 10.5%; Score 127; DB 22; Length 266;
 Best Local Similarity 100.0%; Pred. No. 5.3e-117;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 290 EQKHGFEVASTSPEDSPGSPNPEPATPPQGLRTFDQDLAISLPTSDIFVSYSTFP 349
 Db 140 EQKHGFEVASTSPEDSPGSPNPEPATPPQGLRTFDQDLAISLPTSDIFVSYSTFP 199
 Qy 350 GFVSWRPKSGSMYVETLDDIFQWHSDELQSLLRVANVSKGIYKQMPCCFNFLRK 409
 Db 200 GFVSWRPKSGSMYVETLDDIFQWHSDELQSLLRVANVSKGIYKQMPCCFNFLRK 259
 Qy 410 KLFKFTS 416
 Db 260 KLFKFTS 266
 RESULT 12
 ABJ04760
 ID ABJ04760 standard; protein; 93 AA.
 XX
 AC ABJ04760;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE Caspase-9 protein sequence SEQ ID No 27.
 XX
 KW Intracellular signaling polypeptide; Nod2; Crohn's disease; mutation;
 KW cytosine residue insertion; nuclear factor, NF-B activation; NF-kappa B;
 KW RICK signaling; gene therapy; transgenic plant; plant.
 XX
 OS Homo sapiens.
 XX

PN WO200244426-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 26-OCT-2001; 2001WO-US51068.
 XX
 PR 30-OCT-2000; 2000US-244266P.
 PR 25-APR-2001; 2001US-286316P.
 PR 26-OCT-2001; 2001US-0286316.
 XX
 PA (UNMI) UNIV MICHIGAN.
 PA (UTCH-) UNIV CHICAGO.
 XX
 PI Nunez G, Inohara N, Ogura Y, Cho J, Nicolae DL, Bonen D;
 XX WPI; 2002-547704/58.
 XX
 XX New isolated intracellular signaling polypeptide, termed Nod2, useful
 PT for producing an antibody that recognizes Nod2, and as a target for
 PT screening drugs
 XX
 PS Disclosure; Fig 2; 316pp; English.
 XX
 XX The invention relates to an isolated intracellular signaling polypeptide,
 CC termed Nod2, comprising a sequence of 1007 or 1040 amino acids, given in
 CC the specification. The nucleic acid encoding the isolated protein is
 CC useful for identifying subjects at risk of developing Crohn's disease by
 CC providing a nucleic acid from the subject, where the nucleic acid
 CC comprises a Nod2 gene, and detecting the presence or absence of one or
 CC more variations in the Nod2 gene. Detecting comprises comparing the
 CC sequence of the nucleic acid to a sequence of a wild-type Nod2 nucleic
 CC acid. Detection is accomplished by hybridisation analysis. The method
 CC further comprises determining if the subject is at risk of developing
 CC Crohn's disease based on the presence or absence of the variations, and
 CC determining a genotype relative risk or a population attributable risk
 CC for the subject. The variation is a polymorphism or a mutation,
 CC preferably a cytosine residue insertion, where the mutation causes a
 CC deletion of a Leu-Arg-Arg repeat of Nod2. The variation results in
 CC increased nuclear factor (NF)-B activation. The variation is selected
 CC from the sequences of the Nod2 gene. The isolated protein is selected
 CC as a target for screening drugs that can alter, for example, RICK signaling,
 CC and thus the physiological effects of NF-kappa B. The Nod2 gene is useful
 CC for producing the isolated protein by recombinant techniques, as starting
 CC nucleic acids for directed evolution, for gene therapy, or to decrease
 CC the level of Nod2 protein or mRNA in transgenic plants, plant tissues, or
 CC plant cells as compared to wild-type plants, plant tissues or plant
 CC cells. This sequence represents a Nod2 related protein of the invention.
 XX
 SQ Sequence 93 AA;
 Query Match 22.4%; Score 93; DB 23; Length 93;
 Best Local Similarity 100.0%; Pred. No. 9.5e-84;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDEADRLRLRCRLRLVEELQVDLQDLVLLSRLFRPHMIEDIQRAGSGRRDQARQLII 60
 Db 1 MDEADRLRLRCRLRLVEELQVDLQDLVLLSRLFRPHMIEDIQRAGSGRRDQARQLII 60
 Qy 61 DLETRGSQLPLFISCLEDTGQDMLASFLRTNR 93
 Db 61 DLETRGSQLPLFISCLEDTGQDMLASFLRTNR 93
 RESULT 13
 ABP71130
 ID ABP71130 standard; protein; 42 AA.
 XX
 AC ABP71130;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Mch6 CARD protein fragment.
 XX

W BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 W neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 W antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

S Unidentified.

N WO200295001-A2.

D 28-NOV-2002.

X 21-MAY-2002; 2002WO-US16230.

P 21-MAY-2001; 2001US-292559P.

X (REGC) UNIV CALIFORNIA.

X Rothman JH, Bloss T, Witze E;

X WPI; 2003-167228/16.

X Inhibiting or increasing programmed cell death of a cell, for treating
 T e.g. cancer, comprises upregulating or inhibiting, respectively, the
 T expression or activity of basic transcription factor (BTF3) or its
 T homolog in the cell.

S Examples; Fig 2B; 84pp; English.

X The invention relates to inhibiting or increasing programmed cell death
 C of a cell. The method involves upregulating or inhibiting, respectively,
 C the expression or activity of basic transcription factor (BTF3) or its
 C homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 C for inhibiting or increasing programmed cell death. They are used for
 C screening for an agent that increases or inhibits programmed cell death
 C or pre-screening for an agent that modulates programmed cell death. The
 C screened agent that increases or inhibits programmed cell death, is used
 C for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 C amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 C or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
 C Sequences ABP71124-135 represent peptide fragments various CARD proteins.

X Sequence 42 AA:

Query Match 10.1%; Score 42; DB 24; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.4e-33;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

47 GSGRRDQARQLIIDLETRGSQLPLFISCLDGTQJMLASF 88

1 GSGRRDQARQLIIDLETRGSQLPLFISCLDGTQJMLASF 42

RESULT 14

ABP71113

D ABP71113 standard; peptide; 19 AA.

X AC

X ABP71113;

X 14-APR-2003 (first entry)

X Mch6 protein CARD region fragment.

X BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 X neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 X antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

X Unidentified.

X WO200295001-A2.

X 28-NOV-2002.

X 21-MAY-2002; 2002WO-US16230.

PR 21-MAY-2001; 2001US-292559P.

XX (REGC) UNIV CALIFORNIA.

XX Rothman JH, Bloss T, Witze E;

XX WPI; 2003-167228/16.

XX Inhibiting or increasing programmed cell death of a cell, for treating

PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF3) or its
 PT homolog in the cell.

XX Examples; Fig 2A; 84pp; English.

XX The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF3) or its
 CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
 CC Sequences ABP71106-123 represent CARD regions of various CARD proteins.

SQ Sequence 19 AA;

Query Match 4.6%; Score 19; DB 24; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.2e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 WDVLLSRELFRPHMIEDIQ 44

Db 1 WDVLLSRELFRPHMIEDIQ 19

RESULT 15

AAV21739

ID AAV21739 standard; peptide; 15 AA.

XX AC

XX AAV21739;

XX 10-SEP-1999 (first entry)

XX Conserved peptide sequence of Mch6 (caspase-9).

XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 XX autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 XX tumour cell; myocardial infarction; human.

XX Homo sapiens.

XX WO9935277-A2.

XX 15-JUL-1999.

XX 11-JAN-1999; 99WO-US00632.

XX 09-JAN-1998; 98US-0070987.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 1999-419353/35.

XX New isolated nucleic acid molecule encoding a rev-caspase - used
 PT for screening and identifying inhibitors or enhancers for treating
 PT cancer or autoimmune disease

S Disclosure; Fig 6; 74pp; English.

X The invention relates to nucleic acid molecules encoding rev-caspases.
C Rev-caspases are cysteine proteases that specifically cleave proteins
C after Asp residues and is expressed as a zymogen, in which the small
C subunit is N-terminal to a large subunit. A gene delivery vehicle
C comprising a rev-caspase coding sequence is useful for the treatment of
C cancer, where the gene delivery vehicle is internalised by tumour cells.
C The gene delivery vehicle can also be used to treat autoimmune diseases.
C Cells transfected with a rev-caspase expressing vector can be used in
C identification of inhibitors or enhancers of caspase-mediated apoptosis.
C In vitro translated rev-caspase can be used to identify an inhibitor or
C enhancer of caspase processing activity. Caspase inhibitors are useful
C for treating neurodegenerative diseases as well as for inhibiting
C apoptosis in the heart following myocardial infarction. Sequences
C AAY21734 -AAY21795 represent conserved peptide sequences in various
C caspases.

X Q Sequence 15 AA;

Query Match 3.6%; Score 15; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 350 GFVSWRDPKSGSWYV 364
|||||
DB 1 GFVSWRDPKSGSWYV 15

RESULT 16
AAE08955
D AAE08955 standard; peptide; 15 AA.

QX AAE08955;

QY 15-NOV-2001 (first entry)

QZ Mammalian ced-3 homologue 6 (Mch6) peptide fragment #6.

QW Apoptic protease; mammalian ced-3 homologue 6; Mch6; cancer;
QV aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
QU autoimmune disease; cerebellar degeneration; Alzheimer's disease;
QT cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
QX viral infection; cell death-mediated disease; neuroprotective.

QY Unidentified.

QZ US6271361-B1.

QX 07-AUG-2001.

QY 25-FEB-1999; 99US-0257218.

QZ 29-MAY-1997; 97US-0865579.

QX (UYJE-) UNIV JEFFERSON THOMAS.

QY Alnemri ES, Fernandes-alnemri T, Litwack G;

QZ WPI; 2001-528686/58.

QX New apoptotic genes and their apoptotic protease products, useful for
QY modulating apoptosis for the therapeutic treatment of human diseases,
QZ e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
QX disease -

QY Disclosure; Column 31; 36pp; English.

QX The invention relates to an isolated gene encoding apoptic protease,
QY mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the
QZ aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and
QX protein sequences are useful for modulating apoptosis for the
QY therapeutic treatment of human diseases. Mch6 sequences are useful

CC for upregulating apoptosis (e.g. for treating cancers, autoimmune
CC disease or viral infections) or downregulating apoptosis (e.g. for
CC treating Alzheimer's disease, Parkinson's disease or cerebellar
CC degeneration). The Mch6 sequence is useful for diagnosing, treating
CC or reducing the severity of cell death-mediated diseases, as well as
CC other diseases mediated by either increased or decreased programmed
CC cell death. The present amino acid sequence is Mch6 peptide fragment.

XX SQ Sequence 15 AA;

Query Match 3.6%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 350 GFVSWRDPKSGSWYV 364
|||||
DB 1 GFVSWRDPKSGSWYV 15

RESULT 17

ABJ01243

ID ABJ01243 standard; Peptide; 15 AA.

XX AC ABJ01243;

DT 18-SEP-2002 (first entry)

XX DE Human caspase conserved region SEQ ID NO: 59.

XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;
XX cancer; autoimmune disease; cytostatic; immunosuppressive.

XX OS Homo sapiens.

XX PN US6376226-B1.

XX PD 23-APR-2002.

XX PF 26-APR-2000; 2000US-0561756.

XX PR 09-JAN-1998; 98US-070897P.

XX PR 08-JAN-1999; 99US-0227721.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 2002-451275/48.

XX PT New rev-caspases engineered to contain the small subunit fused in frame
PT N-terminal to the large subunit, which is in reverse order to the wild
PT type caspases, are useful to treat cancer and autoimmune diseases -

XX PS Disclosure; Fig 6; 81pp; English.

XX CC The present invention provides the protein and coding sequences of human
CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
CC can be used in the gene therapy of cancer and autoimmune diseases. The
CC present sequence is a peptide described in the exemplification of the
CC invention.

XX SQ Sequence 15 AA;

Query Match 3.6%; Score 15; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 350 GFVSWRDPKSGSWYV 364
|||||
DB 1 GFVSWRDPKSGSWYV 15

RESULT 18

```

BP71313
D ABP71313 standard; peptide; 15 AA.
X
X ABP71313;
X
X 28-APR-2003 (first entry)
X
X Human caspase-9-pl2 protein N-terminal fragment.
E
X Omi; HtrA2; serine protease; inhibitor of apoptosis protein; IAP;
X caspase; apoptosis; cytostatic; immunosuppressive; neuroprotective;
X vasotrophic; gene therapy; reaper.
X
X Homo sapiens.
X
X WO2003006680-A2.
X
X 23-JAN-2003.
X
X 15-JUL-2002; 2002WO-US22658.
X
X 13-JUL-2001; 2001US-305378P.
X
X 14-DEC-2001; 2001US-340163P.
X
X (UYJE-) UNIV JEFFERSON THOMAS.
X
X Alnemri ES;
X
X WPI; 2003-221760/21.
X
X New Omi nucleic acids and peptides that bin o an inhibitor of
X apoptosis proteins, useful for regulating or altering caspase-mediated
X apoptosis and for treating cancer, tumor, o: autoimmune diseases -
X
X Example 2; Fig 6; 83pp; English.
X
X The invention relates to polynucleotides encoding an Omi (serine
X protease) peptide or polypeptide. The Omi peptide specifically binds to a
X portion of an inhibitor of Apoptosis Protein (IAP). The Omi polypeptide
X induces caspase-independent apoptosis, or fails to have serine protease
X activity. The Omi peptides are useful for regulating or altering
X apoptosis, specifically caspase-mediated apoptosis, and as immunogens for
X raising antibodies. Enhancers of apoptosis are useful for treating
X cancers, tumors or for destroying cells that mediate autoimmune
X diseases. Compositions may also be used for the treatment of diseases
X associated with inappropriate activation of apoptosis such as
X neurodegenerative diseases and ischemic injury. The antibodies can be
X used in isolating Omi peptides, polypeptides and their variants, in
X identifying molecules that interact with Omi peptides and polypeptides,
X and in inhibiting or enhancing the biological activity of Omi peptides
X and polypeptides. Sequences ABP71310-315 represent fragments of various
X IAP-binding proteins, used to determine Omi as a IAP-binding protein.
X
X Query Match 3.6%; Score 15; DB 24; Length 15;
X Best Local Similarity 100.0%; Pred. No. 3.1e-07;
X Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
X
X 316 ATPFQEGRLTFDQLD 330
X |||||||||
X 1 ATPFQEGRLTFDQLD 15
X
X RESULT 19
X AAEO8939
X ID AAEO8939 standard; peptide; 46 AA.
X AC
X AAEO8939;
X
X 15-NOV-2001 (first entry)
X
X Mammalian ced-3 homologue 6 (Mch6) peptide.
X
X Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
X aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
X autoimmune disease; cerebellar degeneration; Alzheimer's disease;
X cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
X viral infection; cell death-mediated disease; neuroprotective.
X
X Unidentified.
X
X US6271361-B1.
X
X 07-AUG-2001.
X
X 25-FEB-1999; 99US-0257218.
X
X 29-MAY-1997; 97US-0865579.
X
X (UYJE-) UNIV JEFFERSON THOMAS.
X
X Alnemri ES, Fernandes-alnemri T, Litwack G;
X
X WPI; 2001-528686/58.
X
X New apoptotic genes and their apoptotic protease products, useful for
X modulating apoptosis for the therapeutic treatment of human diseases,
X e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
X disease -
X
X Example 1; Fig 2; 36pp; English.
X
X The invention relates to an isolated gene encoding apoptotic protease,
X mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the
X aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and
X protein sequences are useful for modulating apoptosis for the
X therapeutic treatment of human diseases. Mch6 sequences are useful
X for upregulating apoptosis (e.g. for treating cancers, autoimmune
X disease or viral infections) or downregulating apoptosis (e.g. for
X treating Alzheimer's disease, Parkinson's disease or cerebellar
X degeneration). The Mch6 sequence is useful for diagnosing, treating
X or reducing the severity of cell death-mediated diseases, as well as
X other diseases mediated by either increased or decreased programmed
X cell death. The present amino acid sequence is Mch6 peptide.
X
X Sequence 46 AA;
X
X Query Match 3.6%; Score 15; DB 22; Length 46;
X Best Local Similarity 100.0%; Pred. No. 8.4e-07;
X Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
X
X 350 GFVSWRDPKSGSWYV 364
X |||||||||
X 32 GFVSWRDPKSGSWYV 46
X
X RESULT 20
X AAM97045
X ID AAM97045 standard; Peptide; 14 AA.
X
X AC
X AAM97045;
X
X 24-JAN-2002 (first entry)
X
X Human peptide #320 encoded by a SNP oligonucleotide.
X
X Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
X neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
X amyloid protein; angiotensin; apoptosis related protein; cadherin;
X cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
X complement related protein; cytochrome; kinesin; cytokine; interferon;
X interleukin; G-protein coupled receptor; thioesterase; inflammation;
X multifactorial disease; autoimmune disease; infection;
X nervous system disease.
X

```

OS Homo sapiens.
 XX WO200147944-A2.
 XX 05-JUL-2001.
 XX 28-DEC-2000; 2000WO-US35498.
 XX 28-DEC-1999; 99US-0173419.
 XX 27-DEC-2000; 2000US-0173419.
 XX (CURA-) CURAGEN CORP.
 XX Shinketsu RA, Leach M;
 XX WPI; 2001-465210/50.
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g.
 XX cancer, autoimmune diseases and infections.
 XX Disclosure: Page 3718; 4143pp; English.
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 XX encoding polymorphic variants of proteins related to amylases, amyloid
 XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 XX polymerase, oncogenes, histones, kinases, colony stimulating factors,
 XX complement related proteins, cytochromes, kinesins, cytokines,
 XX interferons, interleukins, G-protein coupled receptors and thioesterases.
 XX The present sequence is a peptide encoded by one such oligonucleotide.
 XX The oligonucleotides and the peptides encoded by them may be used in the
 XX prevention, diagnosis and treatment of diseases associated with
 XX inappropriate expression of the proteins listed above. Disorders that may
 XX be prevented, diagnosed and/or treated include multifactorial diseases
 XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 XX and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 XX brain, breast, colon and kidney, leukaemia), diseases of the nervous
 XX system and an infection of pathogenic organisms.
 XX Sequence 14 AA:
 XX
 XX Query Match 3.4%; Score 14; DB 22; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 35 FRPHMIEDIQRAGS 48
 XX |||||
 XX DB 1 FRPHMIEDIQRAGS 14
 XX
 XX RESULT 21
 XX AAU08321:
 XX AAU08321 standard; Peptide; 15 AA.
 XX AAU08321:
 XX 04-DEC-2001 (first entry)
 XX Human MCH6 conserved sequence #6.
 XX Human: aspartate-specific cysteine protease; MCH6; neutrotropic;
 XX neuroprotective; anti-Parkinsonian; antianemic; vasotropic; cardiac;
 XX cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
 XX Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 XX cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;
 XX ischaemic injury; myocardial infarction; stroke; reperfusion injury;
 XX amyotrophic lateral sclerosis; conserved sequence.
 XX Homo sapiens.
 XX OS
 XX US2001016345-A1.
 XX PN
 XX XX

PD 23-AUG-2001.
 XX PF 22-DEC-2000; 2000US-0746731.
 XX PR 29-MAY-1997; 97US-0865579.
 XX PR 25-FEB-1999; 99US-0257218.
 XX (ALNE/) ALNEMRI E S.
 XX (FERN/) FERNANDES-ALNEMRI T.
 XX (LITW/) LITWACK G.
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX WPI; 2001-535542/59.
 XX New Mch6 polypeptides and genes encoding the polypeptides useful for
 XX diagnosing, treating or reducing the severity of cell death-mediated
 XX diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
 XX Parkinson's disease
 XX Example 1; Fig 2; 15pp; English.
 XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
 XX homologue 6) an aspartate-specific cysteine protease and the MCH6
 XX polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
 XX to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
 XX death-mediated diseases (i.e. apoptotic) such as neurodegenerative
 XX diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
 XX lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
 XX myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
 XX myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
 XX nucleic acids and polypeptides can also be used to diagnose or generate
 XX reagents to diagnose diseases mediated or characterised by programmed
 XX cell death. A purified recombinant MCH6 protein can be used to measure
 XX hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
 XX a continuous fluorometric assay. The present sequence represents a
 XX conserved sequence from human MCH6 indicating that MCH6 is a member of
 XX the Ced-like subfamily of proteases.
 XX Sequence 15 AA:
 XX
 XX Query Match 2.9%; Score 12; DB 22; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 0.00029;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 350 GFVSWRDPKSGS 361
 XX |||||
 XX DB 1 GFVSWRDPKSGS 12
 XX
 XX RESULT 22
 XX AAW89198
 XX ID AAW89198 standard; Protein; 299 AA.
 XX AC
 XX AAW89198;
 XX 17-MAR-1999 (first entry)
 XX Aspartate-specific cysteine protease, Caspase-1.
 XX Caspase-1; Spodoptera frugiperda; Sf; insect; nuclear immunophilin;
 XX CED-3 subfamily; aspartate-specific cysteine protease; ASCP; apoptosis.
 XX Spodoptera frugiperda.
 XX Key Location/Qualifiers
 XX Cleavage-site 28..29
 XX Cleavage-site 184..185
 XX Cleavage-site 195..196
 XX US5858778-A.
 XX PN
 XX 12-JAN-1999.
 XX PD

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 339 AA;
 XX Query Match 2.4%; Score 11; DB 2; Length 339;
 XX Best Local Similarity 100.0%; Pred. No. 0.04; Indels 0; Gaps 0;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFFIQAC 287
 DB 201 GKPKLFFFIQAC 211
 |||||

RESULT 25
 ABP71122
 ID ABP71122 standard; peptide; 10 AA.

AC ABP71122;
 DT 14-APR 2003 (first entry);
 DE Mch6 protein CARD region fragment.

XX BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 XX neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 KW antirheumatic; antiarthritic; gene therapy; CARD; Mch6.
 XX Unidentified.

XX WO200295001-A2.
 XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US16230.
 XX 21-MAY-2001; 2001US-292559P.

XX (REGC) UNIV CALIFORNIA.
 XX Rothman JH, Bloss T, Witze E;

XX WPI; 2003-167228/16.
 XX Inhibiting or increasing programmed cell death of a cell, for treating

PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF)3 or its
 PT homolog in the cell.

XX Examples; Fig 2A; 84pp; English.

XX The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF)3 or its
 CC homolog in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.

XX Sequences ABP71106-123 represent CARD regions of various CARD proteins.

XX Sequence 10 AA;

Query Match 2.4%; Score 10; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RQARQLIID 61
 |||||

DB 1 RQARQLIID 10

RESULT 26
 AAM68529
 ID AAM68529 standard; Protein; 163 AA.

XX AAM68529;
 AC AAM68529;

DT 06-NOV-2001 (first entry)
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28835.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.
 XX C9-AUG-2001.

XX 30-JAN-2001; 2001WO-US0668.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0214687.
 XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow.

XX Example 4; SEQ ID NO: 28835; 658pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.

XX Sequence 163 AA;

XX Query Match 2.4%; Score 10; DB 22; Length 163;
 XX Best Local Similarity 100.0%; Pred. No. 0.23; Indels 0; Gaps 0;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
 DB 84 KPKLFFFIQAC 93
 |||||

RESULT 27
 ABG38107
 ID ABG38107 standard; Peptide; 163 AA.

XX ABG38107;
 AC ABG38107;

DT 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 27772.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;

W familial idiopathic pulmonary fibrosis; neurofibromatosis;
W tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
W Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
W pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
W pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
W primary ciliary dyskinesia; pulmonary hypertension;
W hyaline membrane disease.

X Homo sapiens.

S WO200186003-A2.

X 15-NOV-2001.

X 30-JAN-2001; 2001WO-US00665.

X 04-FEB-2000; 2000US-180312P.

X 26-MAY-2000; 2000US-207456P.

X 30-JUN-2000; 2000US-0608408.

X 03-AUG-2000; 2000US-0632366.

X 21-SEP-2000; 2000US-234687P.

X 27-SEP-2000; 2000US-236359P.

X 04-OCT-2000; 2000GB-0024263.

X (MOLE-) MOLECULAR DYNAMICS INC.

X Penn SG, Hanzel DK, Chen W, Rank DR;

X WPI; 2002-114183/15.

X Spatially-addressable set of single exon nucleic acid probes, used to
X measure gene expression in human lung samples

X Claim 27: SEQ ID No 27772; 634pp; English.

X The invention relates to a spatially-addressable set of single exon
X nucleic acid probes for measuring gene expression in a sample derived
X from human lung comprising single exon nucleic acid probes having one of
X 12614 nucleic acid sequences mentioned in the specification, or their
X complements or the 12387 open reading frames derived from the 12614
X probes. Also included are a microarray comprising the novel set of
X probes; the novel set of probes which hybridize at high stringency to a
X nucleic acid expressed in the human lung; measuring gene expression in a
X sample derived from human lung, comprising (a) contacting the array with
X a collection of detectably labeled nucleic acids derived from human lung
X mRNA, and (b) measuring the label detectably bound to each probe of
X the array; identifying exons in a eukaryotic genome, comprising
X (a) algorithmically predicting at least one exon from genomic sequences
X of the eukaryote; and (b) detecting specific hybridisation of detectably
X labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
X having a fragment identical to the predicted exon, the probe is included
X in the above mentioned microarray; assigning exons to a single gene,
X comprising (a) identifying exons from genomic sequence by the method
X above and (b) measuring the expression of each of the exons in several
X tissues and/or cell types using hybridisation to a single exon
X microarrays having a probe with the exon, where a common pattern of
X expression of the exons in the tissues and/or cell types indicate; that
X the exons should be assigned to a single gene; a peptide comprising one
X of 12011 sequences, mentioned in the specification, or encoded by the
X probes/open reading frames (ORF). The probes are used for gene
X expression analysis, and for identifying exons in a gene, particularly
X using human lung derived mRNA and for the study of lung diseases
X such as asthma, lung cancer, chronic obstructive pulmonary disease
X (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
X fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
X Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
X haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
X pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
X pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
X and hyaline membrane disease. The present sequence is a peptide/protein
X encoded by a single exon probe of the invention.

X Note: The sequence data for this patent did not form part
X of the printed specification, but was obtained in electronic

CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 163 AA;

Query Match 2.4%; Score 10; DB 23; Length 163;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287

DB 84 KPCLFFIQAC 93

RESULT 28

AA98655
ID AAB98655 standard; protein; 244 AA.

AC AAB98655;

DT 16-AUG-2001 (first entry)

XX Caspase-7.

KW Caspase-1; Protein co-ordinate data; caspase-7; S4 binding region;
KW caspase-3.

OS Unidentified.

PN WO200137194-A2.

PD 25-MAY-2001.

PF 16-NOV-2000; 2000WO-US31602.

PR 16-NOV-1999; 99US-0165797.

PA (VERT-) VERTEX PHARM INC.

PI Wei Y;

DR WPI; 2001-329229/34.

PT Molecule or molecular complex used for drug discovery, comprises a
PT binding pocket of caspase-7 or a homolog having an S4 binding region
PT more hydrophilic than that of caspase-3

PS Example 4; Fig 3; 161pp; English.

XX The present invention relates to a molecule or molecular complex (I)
XX comprising a binding pocket defined by the structure coordinates of
XX caspase-7 amino acids 234, 235, 237, 276, 278, 281, and 284 or a homolog
XX of (I) with a binding pocket having a root mean square deviation from the
XX amino acid backbone atoms of not more than 1.5 Angstrom, where (I) has an
XX S4 binding region that is more hydrophilic than that of caspase-3. The
XX present sequence is caspase-7, which was used in a sequence homology
XX alignment.

XX Sequence 244 AA;

Query Match 2.4%; Score 10; DB 22; Length 244;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287

DB 118 KPCLFFIQAC 127

RESULT 29

AAW15247
ID AAW15247 standard; Protein; 303 AA.

XX

AC AAW15247;
 21-JUL-1997 (first entry)
 Cysteine protease CMH-1.
 Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptosis;
 programmed cell death; cancer; neurodegenerative disease;
 autoimmune disease; gene therapy; diagnosis.
 Homo sapiens.
 Key Location/Qualifiers
 Peptide 1..23
 /label= Pro-peptide
 Protein 24..303
 /label= Mat protein
 /note= "active CMH-1 polypeptide (Claim 3)"
 Protein 29..303
 /label= Mat protein
 /note= "active CMH-1 polypeptide (Claim 3)"
 Active-site 155
 /note= "His144 is a catalytic residue"
 Active-site 186
 /note= "Cys186 is a catalytic residue"
 WO9716552-A1.
 09-MAY-1997.
 01-NOV-1996; 96WO-US17431.
 16-NOV-1995; 95US-0528733.
 03-NOV-1995; 95US-0007211.
 06-NOV-1995; 95US-0007251.
 (VERT-) VERTEX PHARM INC.
 Lippke JA, Su M;
 WPI: 1997-272121/24.
 N-PSDB; AAT66970.
 DNA encoding active, activatable or inactive cysteine protease CMH-1
 - useful in gene therapy for promoting and inhibiting apoptosis and
 for diagnosing cells with potential for apoptosis
 Claim 3; Page 32-33; 48pp; English.
 A proenzyme (AAW15247) is activated to CMH-1, or CPP32/Mch2
 homologue-1, a human cysteine protease that is involved in
 apoptosis. Its amino acid sequence was deduced from a full-length
 isolated cDNA clone (AAT66970). Active, activatable (i.e. proenzyme)
 or inactivated forms of CMH-1 can be expressed in prokaryotic or
 eukaryotic host cells. The polypeptides are useful for screening
 potential apoptosis inhibitors and for raising antibodies used to
 assay CMH-1, to regulate cholesterol levels, in bit CMH-1 activity
 and therefore apoptosis, and to purify CMH-1 polypeptides.
 Sequence 303 AA;
 Query Match 2.4%; Score 10; DB 18; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 278 KPCLFFFIQAC 287
 Db 177 KPCLFFFIQAC 186
 RESULT 30
 AAW15262
 ID AAW15262 standard; Protein; 303 AA.

XX AAW15262;
 05-AUG-1997 (first entry)
 Apototic protease Mch3-alpha.
 Mch3-alpha; cysteine protease; apoptosis; AIDS; ischaemia;
 neurodegenerative disease; therapy; diagnosis.
 Homo sapiens.
 Key Location/Qualifiers
 Domain 1..198
 /label= P20
 /note= p20 subunit
 Domain 199..303
 /label= P12
 /note= p12 subunit
 Cleavage-site 24..28
 /label= P20
 Cleavage-site 54..58
 /label= P17
 Cleavage-site 99..103
 /label= P12
 Active-site 184..188
 /note= "QACRG active site"
 WO9718313-A1.
 22-MAY-1997.
 12-NOV-1996; 96WO-US18118.
 13-NOV-1995; 95US-0556627.
 (IDUN-) IDUN PHARM INC.
 (UYJE-) UNIV JEFFERSON THOMAS.
 Alnemri ES, Armstrong R, Fernandes-Alnemri T, Litwack G;
 Tomaselli K;
 WPI: 1997-289289/26.
 N-PSDB; AAT66992.
 New gene encoding Mch3, a cysteine protease that regulates apoptosis
 - for treating human diseases associated with apoptosis, and
 screening for antagonists and agonists of Mch3
 Claim 8; Fig 1; 52pp; English.
 Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member
 of the interleukin-1-beta converting enzyme (ICE) family of cysteine
 proteases. Its amino acid sequence was deduced from a cDNA clone
 (AAT66992) obtd. from a Jurkat library. Mch3-beta (AAW15263) has also
 been identified that lacks the active site of Mch3-alpha.
 Mch3-alpha polypeptides can be produced in engineered host cells
 and used to treat human diseases associated with cell death, such
 as AIDS, ischaemic injury, neurodegenerative diseases, etc. They
 can also be used to regulate apoptosis and to screen for Mch3
 agonists and antagonists.
 Sequence 303 AA;
 Query Match 2.4%; Score 10; DB 18; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 278 KPCLFFFIQAC 287
 Db 177 KPCLFFFIQAC 186

XX ABJ01222;
XX 18-SEP-2002 (first entry)
XX Human caspase-7 SEQ ID NO: 24.
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis;
XX cancer; autoimmune disease; cytostatic; immunosuppressive.
XX Homo sapiens.
XX US6376226-B1.
XX 23-APR-2002.
XX 26-APR-2000; 2000US-0561756.
XX 09-JAN-1998; 98US-070897P.
XX 08-JAN-1999; 99US-0227721.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Alnemri ES;
XX WPI; 2002-451275/48.
XX N-PSDB; ABT03970.
XX New rev-caspases engineered to contain the small subunit fused in frame
XX N-terminal to the large subunit, which is in reverse order to the wild
XX type caspases, are useful to treat cancer and autoimmune diseases -
XX Disclosure; Fig 17; 81pp; English.
XX The present invention provides the protein and coding sequences of human
XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
XX can be used in the gene therapy of cancer and autoimmune diseases. The
XX present sequence is a protein described in the exemplification of the
XX invention.
XX Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB : ; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.39;
XX Matches 10; Conservative 0; Mismatches ; Indels 0; Gaps 0;
XX
XX QY 278 KPQLFFFIQAC 287
XX 177 KPQLFFFIQAC 186
XX
XX RESULT 34
XX ABB09297
XX ID ABB09297 standard; Protein; 303 AA.
XX AC ABB09297;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human caspase 7 protein sequence SEQ ID NO:3.
XX
XX KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX hyperproliferative disorder; cancer; bone metabolism; infection;
XX cholesterol disorder; inflammation; tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200222640-A1.
XX
XX PD 21-MAR-2002.
XX
XX PF 10-SEP-2001; 2001WO-US28232.
XX

XX 11-SEP-2000; 2000US-0659860.
XX (ISIS-) ISIS PHARM INC.
XX Zhang H, Watt AT;
XX WPI; 2002-401902/43.
XX N-PSDB; ABN80825.
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
XX for modulating gene expression and treating diseases associated with
XX expression of caspase 7 in humans -
XX Example 13; Page 94-96; 138pp; English.
XX The present invention describes a compound (I) 8-50 nucleobases in
XX length targeted to a nucleic acid molecule encoding caspase 7, which
XX specifically hybridises with and inhibits the expression of caspase 7.
XX (I) has antiinflammatory and cytostatic activities, and can be used in
XX antisense therapy and as an inhibitor of caspase 7 expression. (I) is
XX useful for inhibiting the expression of caspase 7 in human cells or
XX tissues, and for treating a human having a disease or condition
XX associated with caspase 7 including inflammatory condition,
XX hyperproliferative disorder (cancer), or bone metabolism or cholesterol
XX disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
XX as research reagent and kits. (I) is useful prophylactically to prevent
XX or delay infection, inflammation or tumour formation. The present
XX sequence represents a human caspase 7 protein, which is used in an
XX example from the present invention.
XX Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB 23; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.39;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 278 KPQLFFFIQAC 287
XX 177 KPQLFFFIQAC 186
XX
XX RESULT 35
XX ABB09299
XX ID ABB09299 standard; Protein; 303 AA.
XX AC ABB09299;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human caspase 7 protein sequence SEQ ID NO:17.
XX
XX KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX hyperproliferative disorder; cancer; bone metabolism; infection;
XX cholesterol disorder; inflammation; tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200222640-A1.
XX
XX PD 21-MAR-2002.
XX
XX PF 10-SEP-2001; 2001WO-US28232.
XX
XX PR 11-SEP-2000; 2000US-0659860.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX Zhang H, Watt AT;
XX WPI; 2002-401902/43.
XX N-PSDB; ABN80839.
XX

SEQ Sequence 308 AA;

Query Match 2.4%; Score 10; DB 22; Length 308;

Best Local Similarity 100.0%; Pred. No. 0.4; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPQLFFIQAC 287
| | | | |
DB 162 KPQLFFIQAC 171

RESULT 38

ABB09300
ID ABB09300 standard; Protein; 336 AA.

AC ABB09300;

DT 15-JUL-2002 (first entry)

DE Human caspase 7 protein sequence SEQ ID NO:18.

DE Caspase 7; antisense modulation; antiinflammatory; cytostatic;
KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
KW hyperproliferative disorder; cancer; bone metabolism; infection;
KW cholesterol disorder; inflammation; tumour.

OS Homo sapiens.

XX WO200222640-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US28232.

XX 11-SEP-2000; 2000US-0659860.

XX (ISIS-) ISIS PHARM INC.

XX Zhang H, Watt AT;

XX WPI; 2002-401902/43.

XX N-PSDB; ABN80840.

XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
PT for modulating gene expression and treating diseases associated with
PT expression of caspase 7 in humans
XX Example 15; Page 103-105; 138pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in
CC length targeted to a nucleic acid molecule encoding caspase 7, which
CC specifically hybridises with and inhibits the expression of caspase 7.
CC (I) has antiinflammatory and cytostatic activities, and can be used in
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
CC useful for inhibiting the expression of caspase 7 in human cells or
CC tissues, and for treating a human having a disease or condition
CC associated with caspase 7 including inflammatory condition.
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
CC as research, reagent and kits. (I) is useful prophylactically to prevent
CC or delay infection, inflammation or tumour formation. The present
CC sequence represents a human caspase 7 protein, which is used in an
CC example from the present invention.

XX Sequence 336 AA;

Query Match 2.4%; Score 10; DB 23; Length 336;

Best Local Similarity 100.0%; Pred. No. 0.43; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPQLFFIQAC 287
| | | | |
DB 210 KPQLFFIQAC 219

RESULT 39

ABB09298
ID ABB09298 standard; Protein; 340 AA.

AC ABB09298;

DT 15-JUL-2002 (first entry)

DE Mouse caspase 7 protein sequence SEQ ID NO:10.

DE Caspase 7; antisense modulation; antiinflammatory; cytostatic;
KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
KW hyperproliferative disorder; cancer; bone metabolism; infection;
KW cholesterol disorder; inflammation; tumour.

OS Mus musculus.

XX WO200222640-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US28232.

XX 11-SEP-2000; 2000US-0659860.

XX (ISIS-) ISIS PHARM INC.

XX Zhang H, Watt AT;

XX WPI; 2002-401902/43.

XX N-PSDB; ABN80832.

XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
PT for modulating gene expression and treating diseases associated with
PT expression of caspase 7 in humans
XX Example 13; Page 97-99; 138pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in
CC length targeted to a nucleic acid molecule encoding caspase 7, which
CC specifically hybridises with and inhibits the expression of caspase 7.
CC (I) has antiinflammatory and cytostatic activities, and can be used in
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
CC useful for inhibiting the expression of caspase 7 in human cells or
CC tissues, and for treating a human having a disease or condition
CC associated with caspase 7 including inflammatory condition.
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
CC as research, reagent and kits. (I) is useful prophylactically to prevent
CC or delay infection, inflammation or tumour formation. The present
CC sequence represents a mouse caspase 7 protein, which is used in an
CC example from the present invention.

XX Sequence 340 AA;

Query Match 2.4%; Score 10; DB 23; Length 340;

Best Local Similarity 100.0%; Pred. No. 0.44; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPQLFFIQAC 287
| | | | |
DB 214 KPQLFFIQAC 223

RESULT 40

AAR95830
ID AAR95830 standard; Protein; 341 AA.

AC AAR95830;

DT 28-OCT-1996 (first entry)

XX Human interleukin-1-converting enzyme-like apoptosis protease-3.
 DE ICE-LAP-3; interleukin-1-converting enzyme-like apoptosis protease;
 XX enzyme; Alzheimer's disease; Parkinson's disease; septic shock;
 KW head injury; rheumatoid arthritis.
 XX Homo sapiens.
 OS WO9613603-A1.
 XX PN 09-MAY-1996.
 XX PD 06-JUN-1995; 95WO-US07235.
 XX PF 01-NOV-1994; 94US-0334251.
 XX PR (HUMA-) HUMAN GENOME SCI INC.
 XX Hastings GA, He W, Hudson PL, Rosen CA;
 DR WPI; 1996-239509/24.
 DR N-PSDB; AAT15276.
 XX Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis
 XX and treatment of Alzheimer's disease, Parkinson's disease,
 XX rheumatoid arthritis, septic shock and head injury
 XX Claim 1; Page 91-92; 67pp; English.
 XX This ICE-LAP-3 protein may be used therapeutically, e.g. as an
 XX antitumor or antiviral agent and to control embryonic development
 XX and tissue homeostasis. The protein can also be used to treat
 XX immunosuppression disorders, such as AIDS, by targeting virus
 XX infected cells for cell death. The DNA may find use in gene
 XX therapy applications.
 XX Sequence 341 AA;
 Q Query Match 2.4%; Score 10; DB 1; Length 341;
 Best Local Similarity 100.0%; Pred. No. 0.44;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 278 KPQLFFFIQAC 287
 b 252 KPQLFFFIQAC 261
 RESULT 41
 LAWS4392
 D AAW54392 standard; Protein; 389 AA.
 X AAW54392;
 C
 X 14-SEP-1998 (first entry)
 X Human LICE3 polypeptide.
 X LICE3; interleukin-1 beta converting enzyme-like cysteine protease;
 W human; apoptosis; agonist; antagonist; cancer; infection; HIV;
 W Parkinson's disease; Alzheimer's disease; autoimmune disease;
 W therapy; diagnosis.
 X Homo sapiens.
 X
 X Key Location/Qualifiers
 R Cleavage-site 85..86
 T /note= "putative cleavage site"
 T Cleavage-site 280..281
 T /note= "putative cleavage site"
 T Cleavage-site 294..295
 T /note= "putative cleavage site"
 T Peptide 266..270

FT /note= "amino acid sequence critical for covalent
 linkage to the substrate"
 XX WO9814598-A1.
 PN 09-APR-1998.
 PD 18-SEP-1997; 97WO-US16841.
 XX PF 01-OCT-1996; 96US-0724378.
 XX PR (AMGE-) AMGEN INC.
 XX Fletcher FA, Juan S, Patterson SD;
 PI WPI; 1998-240097/21.
 XX DR N-PSDB; AAV26613.
 XX New isolated interleukin-1 beta converting enzyme like protease - is
 XX used to develop products for modulating apoptosis, e.g. for treating
 XX cancers, viral infection, nervous system degeneration or autoimmune
 XX disease
 XX Claim 7; Fig 1; 63pp; English.
 XX This polypeptide comprises human LICE3, a novel cysteine protease
 XX having homology to interleukin-1 beta converting enzyme (ICE). Its
 XX amino acid sequence was deduced from a cDNA clone (see AAV26613) from
 XX a human foetal liver library. LICE3 has significant homology to
 XX apoptosis genes ICE and CED-3 and is most closely related to LICE2
 XX (57% homology). The invention provides LICE3 nucleic acids,
 XX vectors and host cells for the expression of LICE. Also disclosed
 XX are LICE3 agonists and antagonists, and methods for treatment of
 XX disorders characterised by altered apoptosis. LICE3 agonists can
 XX be used to treat cancers by promoting apoptosis of tumour cells.
 XX LICE3 antagonists can be used to treat conditions resulting from
 XX increased apoptosis, such as viral infections (e.g. AIDS), nervous
 XX system degeneration (e.g. Parkinson's disease, Alzheimer's disease)
 XX and autoimmune diseases. The products can also be used for
 XX detection and diagnosis.
 XX Sequence 389 AA;
 Q Query Match 2.4%; Score 10; DB 19; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 278 KPQLFFFIQAC 287
 b 259 KPQLFFFIQAC 268
 RESULT 42
 AAW27390
 ID AAW27390 standard; Protein; 479 AA.
 X AAW27390;
 C
 X 25-MAR-2003 (updated)
 DT 09-APR-1998 (first entry)
 XX Mch4 protein.
 DE Mch4; Mch5; aspartic acid specific Cys protease; cell apoptosis; stroke;
 KW increased cell survival; hormone dependent tumour; autoimmune disease;
 KW immunoglobulin mediated glomerulonephritis; degenerative disease;
 KW therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Domain 18..105
 FT /note= "Mch4A domain, no specified function"

Domain 112..189
/note= "Mch4B domain, no specified function"

WO9735020-A1.
25-SEP-1997.
19-MAR-1997; 97WO-US04330.
14-JUN-1996; 96US-0665220.
19-MAR-1996; 96US-0618408.
(IDUN-) IDUN PHARM INC.
(UYJE-) UNIV JEFFERSON THOMAS.
Alnemri ES, Fernandesalnemri T, Litwack G, Armstrong R;
Tomaselli K;
WPI; 1997-480225/44.
N-PSDB; AAT90097.
Aspartic acid specific cysteine protease(s) Mch4 and Mch5 - which
are involved in cell apoptosis, useful to diagnose and treat, e.g.
cancer, autoimmune, Alzheimer's or Parkinson's disease
Claim 10; Fig 1; 76pp; English.
This sequence represents the Mch4 protein, which is an isolated protein of
the invention. Mch4 and Mch5 (see AAW21724) are members of the Aspartic
acid specific Cys protease family involved in cell apoptosis. The genes
and proteins can be used to diagnose, treat or prevent the severity of
diseases resulting from increased cell survival, e.g. hormone dependent
tumours such as breast, prostate or ovarian cancers, or autoimmune
diseases, such as systemic lupus erythematosus or immunoglobulin
mediated glomerulonephritis, diseases resulting from decreased cell
survival, e.g. degenerative diseases such as Alzheimer's or Parkinson's
disease, or amyotrophic lateral sclerosis or other diseases associated
with increased apoptosis such as aplastic anaemia, stroke, ischaemic
injury following myocardial infarction or reperfusion injury.
(Updated on 25-MAR-2003 to correct PI field.)
Sequence 479 AA:
Query Match 2.4%; Score 10; DB 18; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
278 KPQLFFFIQAC 287
|||||
349 KPQLFFFIQAC 358
RESULT 43
AAW76629
D AAW76629 standard; protein; 479 AA.
X C
X C
X C
12-JUL-1999 (first entry)
Human Mch4 protein fragment containing death effector domain.
Death effector domain; human; murine; anti-apoptotic; treatment;
HIV infection; autoimmune disease; Mch4 protein.
Homo sapiens.
DE19713393-A1.
08-OCT-1998.
01-APR-1997; 97DE-1013393.
XX

PR 01-APR-1997; 97DE-1013393.
XX (TSCH/) TSCHOPP J.
PA (APOT-) APOTECH SA.
XX
PI Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;
PI Imler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;
PI Thome M, Tschopp J, Hofmann K;
XX WPI; 1998-532710/46.
XX
XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases
PT
PS Disclosure; Fig 3; 45pp; German.
XX
XX This invention describes novel human and mouse anti-apoptotic gene
CC products which contain at least one death effector domain. The products
CC of the invention are used in the treatment of HIV infections and
CC autoimmune diseases.
XX
SQ Sequence 479 AA:
Query Match 2.4%; Score 10; DB 19; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
278 KPQLFFFIQAC 287
|||||
349 KPQLFFFIQAC 358
RESULT 44
AAW21724
ID AAW21724 standard; Protein; 479 AA.
XX
AC AAW21724;
XX
DT 10-SEP-1999 (first entry)
XX
DE Amino acid sequence of caspase-10 (Mch4).
XX
KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW tumour cell; myocardial infarction; human.
XX
OS Homo sapiens.
XX
PN WO9935277-A2.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-US00632.
XX
PR 09-JAN-1998; 98US-0070987.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 1999-419353/35.
DR N-PSDB; AAX81226.
XX
XX New isolated nucleic acid molecule encoding a rev-caspase - used
PT for screening and identifying inhibitors or enhancers for treating
PT cancer or autoimmune disease
XX
XX Disclosure; Fig 20A-B; 74pp; English.
XX
XX The invention relates to nucleic acid molecules encoding rev-caspases.
CC Rev-caspases are cysteine proteases that specifically cleave proteins
CC after Asp residues and is expressed as a zymogen, in which the small
CC subunit is N-terminal to a large subunit. A gene delivery vehicle

C comprising a rev-caspase coding sequence is useful for the treatment of
 C cancer, where the gene delivery vehicle is internalised by tumour cells.
 C The gene delivery vehicle can also be used to treat autoimmune diseases.
 C Cells transfected with a rev-caspase expressing vector can be used in
 C identification of inhibitors or enhancers of caspase-mediated apoptosis.
 C In vitro translated rev-caspase can be used to identify an inhibitor or
 C enhancer of caspase processing activity. Caspase inhibitors are useful
 C for treating neurodegenerative diseases as well as for inhibiting
 C apoptosis in the heart following myocardial infarction. Sequences
 C AAX81217 - AAX81226 represent human caspase genes encoding caspase 1-10
 C gene products (AAX21715-Y21724).

X Sequence 479 AA;

Query Match 2.4%; Score 10; DB 20; Length 479;

Best Local Similarity 100.0%; Pred. No. 0.59; Length 479;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 278 KPQLFFIQAC 287
 |||||
 b 349 KPQLFFIQAC 358

RESULT 45

AAE00621
 AAE00621 standard; Protein; 479 AA.

AAE00621;

02-JUL-2001 (first entry)

Human caspase-10.

Human; caspase-10; Mch4; urokinase; proliferation; gene therapy;
 cysteine protease; apoptosis; caspase expression cassette; metastasis;
 tumour; cathepsin B.

Homo sapiens.

Key Location/Qualifiers

Cleavage-site 219..220

/label= Proteolytic_cleavage site

Cleavage-site 372..373

/label= Proteolytic_cleavage site

W0200129232-A2.

26-APR-2001.

19-OCT-2000; 2000MO-US28941.

20-OCT-1999; 99US-0160559.

14-AUG-2000; 2000US-0225564.

(SCIO-) SCIOS INC.

Cordell B, Li Y;

WPI; 2001-290920/30.

N-PSDB; AAD03917.

Novel fusion polypeptide comprising first and second caspase subunit
 separated by cleavage site not associated in nature with caspase
 subunit; useful for cloning gene encoding enzymes involved in
 proteolytic cleavage.

Claim 4: Page 108-110; 116pp; English.

The present amino acid sequence is human Caspase-10 also known as
 Mch4. Caspases are a family of cysteine proteases, that participate in
 the initiation and execution of apoptosis. Caspases exist as pro-enzymes,
 activated by cleavage into a large and small subunit, occurring after
 specific aspartic acid residues within the pro-enzyme sequence.

CC The present invention relates to a method for functional cloning of genes
 CC encoding proteins or enzymes involved in proteolytic cleavage. The
 CC invention is based on the use of caspase expression cassettes comprising
 CC the coding sequence of a proteolytic cleavage site flanked by sequences
 CC encoding two caspase subunits. A fusion polypeptide comprising a first
 CC and a second caspase subunit, separated by a cleavage site not associated
 CC in nature, is useful for cloning gene encoding enzymes involved in
 CC proteolytic cleavage. An expression cassette containing fusion
 CC polypeptide is used to identify a mutant cell line deficient in an
 CC enzyme of interest and is also useful for diagnosis and suppression of
 CC proliferation or metastases of a tumour cell characterised by
 CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
 CC selectively expressed in the tumour cells). DNA encoding fusion
 CC polypeptide is used in gene therapy.
 CC Note: This sequence SEQ.ID.NO.20 is stated as being the same as that
 CC shown in Figure 20 (See AAE00607) in the specification. However these
 CC sequences differ at several positions.

XX Sequence 479 AA;

Query Match 2.4%; Score 10; DB 22; Length 479;

Best Local Similarity 100.0%; Pred. No. 0.59;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPQLFFIQAC 287

Db 349 KPQLFFIQAC 358

RESULT 46

ABJ01225
 ID ABJ01225 standard; Protein; 479 AA.

XX ABJ01225;

DT 18-SEP-2002 (first entry)

Human caspase-10 SEQ ID NO: 33.

Human; caspase; rev-caspase; gene therapy; protease; apoptosis;
 cancer; autoimmune disease; cytostatic; immunosuppressive.

Homo sapiens.

US6376226-B1.

23-APR-2002.

26-APR-2000; 2000US-0561756.

09-JAN-1998; 98US-070897P.

08-JAN-1999; 99US-0227721.

(UYJE-) UNIV JEFFERSON THOMAS.

Alnemri ES;

WPI; 2002-451275/48.

N-PSDB; ABT03973.

New rev-caspases engineered to contain the small subunit fused in frame
 PT N-terminal to the large subunit, which is in reverse order to the wild
 PT type caspases, are useful to treat cancer and autoimmune diseases.
 XX Disclosure; Fig 20; 81pp; English.

XX The present invention provides the protein and coding sequences of human

CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
 CC can be used in the gene therapy of cancer and autoimmune diseases. The
 CC present sequence is a protein described in the exemplification of the
 CC invention.

XX Sequence 479 AA;

Query Match 2.4%; Score 10; DB 23; Length 479;
Best Local Similarity 100.0%; Pred.No. 0.59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 349 KPKLFFFIQAC 358

RESULT 47
AAW50007
ID AAW50007 standard; Protein; 521 AA.

XX AC AAW50007;
XX DT 11-JUN-1998 (first entry)
XX DE Human protease FMH-1.

XX QW Human; protease FMH-1; interleukin-1 beta converting enzyme;
XX QW ICE/CED3-like protease; apoptosis induction;
XX QW apoptosis inhibition.

XX QX Homo sapiens.
XX QX WO9800554.A1.
XX QX 08-JAN-1998.

XX QX 02-JUL-1997; 97MO-US11590.

XX QX 03-JUL 1996; 96US-0675123.

XX QX (GENY) GENETICS INST INC.

XX QX Bowman MR;

XX QX WPI; 1998 086979/08.
XX QX N-PSDB; AAV18R19.

XX QX Isolated nucleic acid encoding human FMH-1 protein - useful for
XX QX treating conditions associated with failed or excess apoptosis e.g.
XX QX cancer and neurological diseases

XX QX Claim 9; Pages 16-18; 29pp; English.

XX QX The present sequence is the human protease FMH-1, which is an
XX QX interleukin-1 beta converting enzyme (ICE)/CED3-like protease.
XX QX FMH-1 can be used to induce apoptosis, while fragments may
XX QX induce or inhibit apoptosis depending on which FMH-1 region they
XX QX bind. Peptide mimetics or small molecule inhibitors targetted to
XX QX FMH-1 can have the same effects. Induction of apoptosis can be
XX QX used, e.g. to treat autoimmune disease, cancer and persistent
XX QX infections, while its inhibition is used to treat
XX QX neurodegeneration, e.g. Alzheimer's, Parkinson's or Huntington's
XX QX diseases, or ischaemic damage, also to increase response to weakly
XX QX immunogenic antigens. FMH-1 can also be used to generate
XX QX antibodies for therapeutic use by blocking binding of ligands to
XX QX FMH-1.

XX QX Sequence 521 AA;

Query Match 2.4%; Score 10; DB 16; Length 521;
Best Local Similarity 100.0%; Pred.No. 0.63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

yy 278 KPKLFFFIQAC 287
| | | | | | | | | |
b 392 KPKLFFFIQAC 401

RESULT 48

AAE00607
ID AAE00607 standard; Protein; 521 AA.

XX AC AAE00607;

XX DT 02-JUL-2001 (first entry)

XX DE Human caspase-10, alternative version.

XX QW Human; caspase-10; Mch4; urokinase; proliferation; gene therapy;
XX QW cysteine protease; apoptosis; caspase expression cassette; metastasis;
XX QW tumour; cathepsin B.

XX QX Homo sapiens.

XX QX Key Location/Qualifiers

XX FT Misc-difference 68 /note= "Encoded by GAG"

XX FT Cleavage-site 219..220

XX FT /label= Proteolytic_cleavage_site

XX FT Misc-difference 228..272 /note= "Encoded by CCGAGG"

XX FT Cleavage-site 415..416

XX FT /label= Proteolytic_cleavage_site

XX FT Misc-difference 472..521

XX FT /note= "Encoded by AGA"

XX QX WO200129232-A2.

XX QX 26-APR-2001.

XX QX 19-OCT-2000; 2000WO-US28941.

XX QX 20-OCT-1999; 99US-0160559.

XX QX 14-AUG-2000; 2000US-0225564.

XX QX (SCIO-) SCIOS INC.

XX QX Cordell B, Li Y;

XX QX WPI; 2001-290920/30.

XX QX N-PSDB; AAB03917.

XX PT Novel fusion polypeptide comprising first and second caspase subunit
XX PT separated by cleavage site not associated in nature with caspase
XX PT subunit, useful for cloning gene encoding enzymes involved in
XX PT proteolytic cleavage

XX QX Claim 4; Fig 20; 116pp; English.

XX CC The present sequence is human Caspase-10 alternative version, also known
XX CC as Mch4. Caspases are a family of cysteine proteases, that participate in
XX CC the initiation and execution of apoptosis. Caspases exist as pro-enzymes,
XX CC activated by cleavage into a large and small subunit, occurring after
XX CC specific aspartic acid residues within the pro-enzyme sequence.
XX CC The present invention relates to a method for functional cloning of genes
XX CC encoding proteins or enzymes involved in proteolytic cleavage. The
XX CC invention is based on the use of caspase expression cassettes comprising
XX CC the coding sequence of a proteolytic cleavage site flanked by sequences
XX CC encoding two caspase subunits. A fusion polypeptide comprising a first
XX CC and a second caspase subunit, separated by a cleavage site not associated
XX CC in nature, is useful for cloning gene encoding enzymes involved in
XX CC proteolytic cleavage. An expression cassette containing fusion
XX CC polypeptide is used to identify a mutant cell line deficient in an
XX CC enzyme of interest and is also useful for diagnosis and suppression of
XX CC proliferation or metastases of a tumour cell characterised by
XX CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
XX CC selectively expressed in the tumour cells). DNA encoding fusion
XX CC polypeptide is used in gene therapy.
XX CC Note: This sequence SEQ.ID.NO.20 is stated as being the same as that
XX CC shown in page 108-110 (See AAE00621) in the specification. However these
XX CC sequences differ at several positions.

SQ Sequence 521 AA;

Query Match 2.4%; Score 10; DB 22; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPKLFFIOAC 287
| | | | | | | | | |
DB 392 KPKLFFIOAC 401

RESULT 49

AAAY21736
ID AAY21736 standard; peptide; 9 AA.

XX AC AAY21736;
XX 10-SEP-1999 (first entry)
DE Conserved peptide sequence of Mch6 (caspase-9).
XX KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW tumour cell; myocardial infarction; human.
XX OS Homo sapiens.
XX KW WO9935277-A2.
XX 15-JUL-1999.
XX 11-JAN-1999; 99WO-US00632.
XX 09-JAN-1998; 98US-0070987.
XX (UYJE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES;

DR WPI; 1999-419353/35.

XX New isolated nucleic acid molecule encoding a rev-caspase - used
PT for screening and identifying inhibitors or enhancers for treating
PT cancer or autoimmune disease
XX Disclosure: Fig 6; 74pp; English.
XX The invention relates to nucleic acid molecules encoding rev-caspases.
XX Rev-caspases are cysteine proteases that specifically cleave proteins.
XX after Asp residues and is expressed as a zymogen, in which the small
XX subunit is N-terminal to a large subunit. A gene delivery vehicle
XX comprising a rev-caspase coding sequence is useful for the treatment of
XX cancer, where the gene delivery vehicle is internalised by tumour cells.
XX The gene delivery vehicle can also be used to treat autoimmune diseases.
XX Cells transfected with a rev-caspase expressing vector can be used in
XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
XX In vitro translated rev-caspase can be used to identify an inhibitor or
XX enhancer of caspase processing activity. Caspase inhibitors are useful
XX for treating neurodegenerative diseases as well as for inhibiting
XX apoptosis in the heart following myocardial infarction. Sequences
XX AAY21734 -AAY21795 represent conserved peptide sequences in various
XX caspases.

XX Sequence 9 AA;

Query Match 2.2%; Score 9; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 283 FIOACGGEQ 291

| | | | | | | | | |
b 1 FIOACGGEQ 9

RESULT 50

AAE08952
ID AAE08952 standard; peptide; 9 AA.

XX AC AAE08952;
XX 15-NOV-2001 (first entry)
XX Mammalian ced-3 homologue 6 (Mch6) peptide fragment #3.

XX KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
KW viral infection; cell death-mediated disease; neuroprotective.

OS Unidentified.

XX US6271361-B1.

XX 07-AUG-2001.

XX 25-FEB-1999; 99US-0257218.

XX 29-MAY-1997; 97US-0865579.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-a.nemri T, Litwack G;

XX WPI; 2001-528686/58.

XX New apoptotic genes and their apoptotic protease products, useful for
PT modulating apoptosis for the therapeutic treatment of human diseases,
PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
PT disease -
XX Disclosure: Column 29; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease,

XX mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the
XX aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and
XX protein sequences are useful for modulating apoptosis for the
XX therapeutic treatment of human diseases. Mch6 sequences are useful
XX for upregulating apoptosis (e.g. for treating cancers, autoimmune
XX disease or viral infections) or downregulating apoptosis (e.g. for
XX treating Alzheimer's disease, Parkinson's disease or cerebellar
XX degeneration). The Mch6 sequence is useful for diagnosing, treating
XX or reducing the severity of cell death-mediated diseases, as well as
XX other diseases mediated by either increased or decreased programmed
XX cell death. The present amino acid sequence is Mch6 peptide fragment.

XX Sequence 9 AA;

Query Match 2.2%; Score 9; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 283 FIOACGGEQ 291

| | | | | | | | | |
DB 1 FIOACGGEQ 9

Search completed: October 20, 2003, 12:24:49

Job time : 86 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 20, 2003, 12:27:12 ; Search time 67 Seconds
(without alignments)
1017.754 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 416
Sequence: 1 MDEADRLRLRCLRLVEEL.....YKMPGCFNLRKLLFFNTS 416

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 609560 seqs, 163917102 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609560

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : Published Applications AA:
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2: /cgn2_6/prodata/2/pubpaa/US02_PUBCOMB.pep.*
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9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US11_PUBCOMB.pep.*
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14: /cgn2_6/prodata/2/pubpaa/US14_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US15_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US16_PUBCOMB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US17_PUBCOMB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US18_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	219	52.6	416	10	US-09-954-697-30
2	219	52.6	416	14	US-10-068-569-1
3	195	46.9	416	12	US-09-851-873-102
4	195	46.9	416	12	US-10-141-618-4
5	195	46.9	416	14	US-10-059-749-2
6	93	22.4	93	12	US-10-314-506-77
7	93	22.4	93	14	US-10-014-269-77
8	93	22.4	93	14	US-10-002-974-27
9	42	10.1	42	15	US-10-153-344-26
10	32	7.7	32	14	US-10-068-569-18
11	32	7.7	32	14	US-10-068-569-22
12	19	4.6	19	15	US-10-153-344-16
13	15	3.6	15	10	US-09-954-697-59
14	15	3.6	15	14	US-10-068-569-6
15	15	3.6	15	14	US-10-068-569-11

ALIGNMENTS

16	15	3.6	15	14	US-10-059-749-22	Sequence 22, Appl
17	15	3.6	15	15	US-10-174-105A-131	Sequence 131, App
18	15	3.6	15	15	US-10-174-105A-132	Sequence 132, App
19	15	3.6	15	15	US-10-174-105A-176	Sequence 176, App
20	15	3.6	15	15	US-10-197-634-7	Sequence 7, Appl
21	15	3.6	15	15	US-10-059-749-6	Sequence 6, Appl
22	12	2.9	13	15	US-10-174-105A-133	Sequence 133, App
23	12	2.9	13	15	US-10-174-105A-134	Sequence 134, App
24	10	2.4	10	15	US-10-153-344-17	Sequence 17, Appl
25	10	2.4	10	15	US-09-989-903-38	Sequence 38, Appl
26	10	2.4	10	15	US-10-068-564-38	Sequence 38, Appl
27	10	2.4	10	15	US-09-864-761-47950	Sequence 47950, A
28	10	2.4	10	15	US-09-895-263-2	Sequence 2, Appl
29	10	2.4	303	10	US-09-944-851-2	Sequence 24, Appl
30	10	2.4	303	10	US-09-954-697-24	Sequence 100, App
31	10	2.4	303	12	US-09-851-873-100	Sequence 4, Appl
32	10	2.4	303	12	US-10-280-670-4	Sequence 2, Appl
33	10	2.4	303	15	US-10-137-060-2	Sequence 2, Appl
34	10	2.4	389	12	US-10-280-670-2	Sequence 3, Appl
35	10	2.4	389	12	US-10-280-670-3	Sequence 2, Appl
36	10	2.4	479	9	US-09-952-768-2	Sequence 33, Appl
37	10	2.4	479	11	US-09-954-697-33	Sequence 4, Appl
38	10	2.4	479	11	US-09-009-893-4	Sequence 2, Appl
39	10	2.4	521	9	US-09-962-834A-2	Sequence 103, App
40	10	2.4	521	12	US-09-851-873-103	Sequence 2, Appl
41	10	2.4	521	12	US-10-439-676-2	Sequence 21, Appl
42	10	2.4	571	9	US-09-410-194-21	Sequence 19, Appl
43	9	2.2	9	10	US-09-954-697-56	Sequence 16, Appl
44	9	2.2	9	14	US-10-059-749-19	Sequence 59, App
45	9	2.2	481	9	US-09-410-194-12	Sequence 12, Appl
46	9	2.2	481	9	US-09-410-194-19	Sequence 19, Appl
47	9	2.2	484	14	US-10-005-921-2	Sequence 2, Appl
48	9	2.2	1196	11	US-09-823-394-2	Sequence 24, App
49	8	1.9	579	16	US-10-080-170-212	Sequence 12, Appl
50	7	1.7	7	10	US-09-965-967-12	Sequence 25, Appl
51	7	1.7	7	12	US-10-293-371-2	Sequence 2, Appl
52	7	1.7	7	12	US-10-293-371-25	Sequence 46, Appl
53	7	1.7	7	12	US-10-293-371-46	Sequence 96, Appl
54	7	1.7	25	9	US-09-729-835-96	Sequence 47853, A
55	7	1.7	84	9	US-09-864-761-47853	Sequence 2, Appl
56	7	1.7	101	14	US-10-004-381-2	Sequence 36311, A
57	7	1.7	126	9	US-09-864-761-36311	Sequence 20, Appl
58	7	1.7	133	12	US-10-311-879-20	Sequence 90, Appl
59	7	1.7	202	9	US-09-729-835-90	Sequence 15, Appl
60	7	1.7	224	10	US-09-920-395A-15	Sequence 654, App
61	7	1.7	269	9	US-09-764-853-654	Sequence 63, Appl
62	7	1.7	364	15	US-10-213-990-63	Sequence 849, App
63	7	1.7	368	9	US-09-925-299-849	Sequence 849, App
64	7	1.7	368	11	US-09-925-299-849	Sequence 1388, Ap
65	7	1.7	394	9	US-09-769-970-2	Sequence 2, Appl
66	7	1.7	448	12	US-09-909-320-132	Sequence 132, App
67	7	1.7	490	10	US-09-909-088B-132	Sequence 132, App
68	7	1.7	490	10	US-09-905-291A-132	Sequence 132, App
69	7	1.7	490	10	US-09-902-853-132	Sequence 132, App
70	7	1.7	490	10	US-09-907-824-132	Sequence 132, App
71	7	1.7	490	10	US-09-907-841-132	Sequence 132, App
72	7	1.7	490	11	US-09-904-011-132	Sequence 132, App
73	7	1.7	490	11	US-09-906-742-132	Sequence 132, App
74	7	1.7	490	11	US-09-906-838-132	Sequence 132, App
75	7	1.7	490	11	US-09-906-838-132	Sequence 132, App

RESULT 1

US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF

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; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-697-30

Query Match      52.6%; Score 219; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.7e-200;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 HFVVEVKGD1:AKKMYLALLELARODHGALDCCVVVILSHGCOASHLOFPGAVYGTDCGP 257
Db 198 HFVVEVKGDLTAKMYLVALLLELARODHGALDCCVVVILSHGCOASHLOFPGAVYGTDCGP 257

Qy 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVASTSPEDSPGSNPEPAT 317
Db 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVASTSPEDSPGSNPEPAT 317

Qy 318 PFQEGRLTFDQLDAISSLTPSPDIFVSYSTFPGFV 4RDPKSGSWYVETLDDIFEQWAHS 377
Db 318 PFQEGRLTFDQLDAISSLTPSPDIFVSYSTFPGFV 4RDPKSGSWYVETLDDIFEQWAHS 377

Qy 378 EDLQSLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db 378 EDLQSLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 2
US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/069,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569 1

Query Match      52.6%; Score 219; DB 1; Length 416;
Best Local Similarity 99.7%; Pred. No. 6.7e-20;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 97 KLSKPTLENLTPVLRPEIRKPEVLRPETPRPV1:GSGGFGDVGALESRLGNADLAYILS 156
Db 97 KLSKPTLENLTPVLRPEIRKPEVLRPETPRPV1:GSGGFGDVGALESRLGNADLAYILS 156

Qy 157 MEPGCHLIINNINFCRESGLRTRTGSNDCEKLRBRRESSLHFMVEVKGDLTAKKMWLAL 216
Db 157 MEPGCHLIINNINFCRESGLRTRTGSNDCEKLRBRRESSLHFMVEVKGDLTAKKMWLAL 216

Qy 217 LELARODHGALDCCVVVILSHGCOASHLOFPGAVYGTDCGPVSVEKIVN:ENGTSCPSLG 276
Db 217 LELARODHGALDCCVVVILSHGCOASHLOFPGA: TDGCPVSVEKIVNENGTSCPSLG 276

Qy 277 GKPKLFFIQACGGEQKHGFVASTSPEDSPGSNPEPATPFQEGRLTFDQLDAISSLP 336
Db 277 GKPKLFFIQACGGEQKHGFVASTSPEDSPGSNPEPATPFQEGRLTFDQLDAISSLP 336
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Qy 337 TPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLOSLLLRVANAVSVKGI 396
Db 337 TPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLOSLLLRVANAVSVKGI 396

Qy 397 YKQMPGCFNFKLFFKTS 416
Db 397 YKQMPGCFNFKLFFKTS 416

RESULT 3
US-09-851-873-102
; Sequence 102, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Welland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-102

Query Match      46.9%; Score 195; DB 12; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.7e-177;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 QKHGALDCCVVVILSHGCOASHLOFPGAVYGTDCGPVSVEKIVNIFNGTSCPSLGGKPKL 281
Db 222 QKHGALDCCVVVILSHGCOASHLOFPGAVYGTDCGPVSVEKIVNIFNGTSCPSLGGKPKL 281

Qy 282 FFIQACGGEQKHGFVASTSPEDSPGSNPEPATPFQEGRLTFDQLDAISSLTPSDI 341
Db 282 FFIQACGGEQKHGFVASTSPEDSPGSNPEPATPFQEGRLTFDQLDAISSLTPSDI 341

Qy 342 FVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLOSLLLRVANAVSVKGIYKQMP 401
Db 342 FVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLOSLLLRVANAVSVKGIYKQMP 401

Qy 402 GCFNFKLFFKTS 416
Db 402 GCFNFKLFFKTS 416

RESULT 4
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-141-618-4

Query Match 46.9%; Score 195; DB 12; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.7e-177;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVKEIWNIFNGTSCPSLGGKPKL 281
DB 222 QDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVKEIWNIFNGTSCPSLGGKPKL 281

QY 282 FFIQACGGEQKDHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQDLDAISSLPTPSDI 341
DB 282 FFIQACGGEQKDHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQDLDAISSLPTPSDI 341

QY 342 FVSYSTFGFVSWRDPKSGSNVYVETLDDIFQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401
DB 342 FVSYSTFGFVSWRDPKSGSNVYVETLDDIFQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401

QY 402 GCFNLRKKLFFKTS 416
DB 402 GCFNLRKKLFFKTS 416

RESULT 5

US-10-059-749-2

; Sequence 2, Application US/10059749
; Publication No. JS20020181504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Applicant: Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

IS-10-059-749-2

Query Match 46.9%; Score 195; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.7e-177;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVKEIWNIFNGTSCPSLGGKPKL 281
DB 222 QDHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCVSVKEIWNIFNGTSCPSLGGKPKL 281

QY 282 FFIQACGGEQKDHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQDLDAISSLPTPSDI 341
DB 282 FFIQACGGEQKDHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQDLDAISSLPTPSDI 341

QY 342 FVSYSTFGFVSWRDPKSGSNVYVETLDDIFQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401
DB 342 FVSYSTFGFVSWRDPKSGSNVYVETLDDIFQWHAHSEDLSLLLRVANAVSVKGIYKOMP 401

QY 402 GCFNLRKKLFFKTS 416
DB 402 GCFNLRKKLFFKTS 416

RESULT 6

US-10-314-506-27

; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,211
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,211
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27

Query Match 22.4%; Score 93; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRRLLRRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGRRDQARQLII 60
DB 1 MDEADRRLLRRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGRRDQARQLII 60

QY 61 DLETRGSOALPLFISCLDGTQDMLASFLRTNR 93
DB 61 DLETRGSOALPLFISCLDGTQDMLASFLRTNR 93

RESULT 7

US-10-014-269-27

; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

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Query Match      22.4%; Score 93; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELFPRPHMIEDIORAGSGSRDQAROLII 60
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Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELFPRPHMIEDIORAGSGSRDQAROLII 60
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QY 61 DLETRGSQALPLFISCLDGTGDMLASFLRTNR 9;
   |||||
Db 61 DLETRGSQALPLFISCLDGTGDMLASFLRTNR 93

RESULT 8
US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Oguri, Yasuhiro
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10-002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27

Query Match      22.4%; Score 93; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELFPRPHMIEDIORAGSGSRDQAROLII 60
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QY 61 DLETRGSQALPLFISCLDGTGDMLASFLRTNR 93
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Db 61 DLETRGSQALPLFISCLDGTGDMLASFLRTNR 93

RESULT 9
US-10-153-344-26
; Sequence 26, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: BLOSS, TIM
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS1
; FILE REFERENCE: 4077-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 26
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-153-344-26

Query Match      10.1%; Score 42; DB 15; Length 42;
```

```
Best Local Similarity 100.0%; Pred. No. 2.6e-32;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GSGSRDQARQLIIDLETRGSQALPLFISCLDGTGDMLASF 88
   |||||
Db 1 GSGSRDQARQLIIDLETRGSQALPLFISCLDGTGDMLASF 42
   |||||

RESULT 10
US-10-068-569-18
; Sequence 18, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-18

Query Match      7.7%; Score 32; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.8e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 PEDESPGSNPEDATPFQEGURTFDQLDAISS 334
   |||||
Db 1 PEDESPGSNPEDATPFQEGURTFDQLDAISS 32
   |||||

RESULT 11
US-10-068-569-22
; Sequence 22, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-22

Query Match      7.7%; Score 32; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.8e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 PEDESPGSNPEDATPFQEGURTFDQLDAISS 334
   |||||
Db 1 PEDESPGSNPEDATPFQEGURTFDQLDAISS 32
   |||||

RESULT 12
US-10-153-344-16
; Sequence 16, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
```

APPLICANT: ROTHMAN, JOEL
APPLICANT: BLOSS, TIM
APPLICANT: WITZE, ERIC
TITLE OF INVENTION: BIF3: AN INHIBITOR OF APOPTOSIS
FILE REFERENCE: 407T-300410US
CURRENT APPLICATION NUMBER: US/10/153,344
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US 60/292,559
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent in version 3.0
SEQ ID NO 16
LENGTH: 19
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-153-344-16

Query Match 4.6%; Score 19; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 WDVLLSRELFRPHWIEDIQ 44
Db 1 WDVLLSRELFRPHWIEDIQ 19

RESULT 13
US-09-954-697-59
Sequence 59, Application US/09954697
Publication No. US20020106631A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASE
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-09-954-697-59

Query Match 3.6%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 14
US-10-068-569-6
Sequence 6, Application US/10068569
Publication No. US20020160975A1
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens

US-10-068-569-6

Query Match 3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFOEGLRTFDOLD 330
Db 1 ATPFOEGLRTFDOLD 15

RESULT 15
US-10-068-569-11
Sequence 11, Application US/10068569
Publication No. US20020160975A1
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-068-569-11

Query Match 3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFOEGLRTFDOLD 330
Db 1 ATPFOEGLRTFDOLD 15

RESULT 16
US-10-059-749-22
Sequence 22, Application US/10059749
Publication No. US20020183504A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

```

:      REGISTRATION NUMBER: 11,815
:      REFERENCE/DOCKET NUMBER: P-ID 2180
:
:      TELECOMMUNICATION INFORMATION:
:
:      TELEPHONE: (619) 535-9001
:      TELEFAX: (619) 535-9849
:
:      INFORMATION FOR SEQ ID NO: 22:
:      SEQUENCE CHARACTERISTICS:
:          LENGTH: 15 amino acids
:          TYPE: amino acid
:          TOPOLOGY: linear
:      MOLECULE TYPE: peptide
:      SEQUENCE DESCRIPTION: SEQ ID NO: 22:
:
:      US-10-059-749-22

```

```
Query Match      3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 350 GFVSWRDPKSGSWYV 364
|||
Db 1 GFVSWRDPKSGSWYV 15

```

RESULT 17
US-10-174-105A-131
: Sequence 131, Application US/10174105A
: Publication No. US20030068652A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signaling Technology, Inc.
: APPLICANT: ZHANG, Hui
: APPLICANT: COMB, Michael J.
: APPLICANT: TAN, Yi
: TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
: TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
: FILE REFERENCE: CST-138 CIP3
: CURRENT APPLICATION NUMBER: US/10/174,105A
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: US 09/148,712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535,364
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 193
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 131
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Peptide
: FEATURE:
: NAME/KEY: MOD_RES
: LOCATION: (101..103)
: OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-131

```

CY 187 CEKLRRRFSSLHFMV 201
DZ 187 CEKLRRRFSSLHFMV 15

RESULT 18
US-10-174-105A-132
; Sequence 132, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi

```

; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-174-105A-132

```

Qy 187 CEKLRRRFSSSLHFNV 201
 |||||
 Db 1 CEKLRRRFSSSLHFNV 15

```

RESULT 19
US-10-174-105A-176
; Sequence 176, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-16
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (107)..(110)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-176

```

Qy 187 CEKLRRRFSSLHFMV 201
 |||||
 Db 1 CEKLRRRFSSLHFMV 15

RESULT 20
US-10-197-634-7
; Sequence 7, Application US/10197634
; Publication No. US20030073629A1

GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
; FILE REFERENCE: IAP-CASPASE INTERACTION
; FILE REFERENCE: 480140.479
; CURRENT APPLICATION NUMBER: US/10/197,634
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-7

Query Match 3.6%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFOEGLRTFDQLD 332
Db 1 ATPFOEGLRTFDQLD 15

RESULT 21
US-10-059-749-6
; Sequence 6, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-059-749-6

Query Match 3.6%; Score 15; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 22
US-10-174-105A-133
; Sequence 133, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-133

Query Match 2.9%; Score 12; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SGLRTRTGSNID 186
Db 2 SGLRTRTGSNID 13

RESULT 23
US-10-174-105A-134
; Sequence 134, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide

US-10-174-105A-134

Query Match 2.9%; Score 12; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 SGLRTRGSNID 186
| | | | | | | | | | | | | | |
Db 2 SGLRTRGSNID 13

RESULT 24

US-10-153-344-17
; Sequence 17, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153.344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-153-344-17

Query Match 2.4%; Score 10; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 RDQARQLIID 61
| | | | | | | | | | | | | | |
Db 1 RDQARQLIID 10

RESULT 25

US-09-989 903-38
; Sequence 38, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-989-903-38

Query Match 2.4%; Score 10; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFFIQAC 287
| | | | | | | | | | | | | | |
Db 21 KPCLFFFIQAC 30

RESULT 26

US-10-068-564-38

; Sequence 38, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-564-38

Query Match 2.4%; Score 10; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPCLFFFIQAC 287
| | | | | | | | | | | | | | |
Db 21 KPCLFFFIQAC 30

RESULT 27

US-09-864-761-47950
; Sequence 47950, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21

;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 47950
;; LENGTH: 163
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007283.3
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
;; OTHER INFORMATION: EST HUMAN HIT: BE271526.1, EVALUE 4.00e-31
;; OTHER INFORMATION: SWISSPROT HIT: Q92851, EVALUE 3.00e-94
US-09-864-761-47950

Query Match 2.4%; Score 10; DB 9; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFQAC 287
| | | | | | | | | |
DB 84 KPCLFFQAC 93

RESULT 28
US-09-895-263-2
;; Sequence 2, Application US/09895263
;; Patent No. US20020076793A1
;; GENERAL INFORMATION:
;; APPLICANT: He, Wei-Wu et al.
;; TITLE OF INVENTION: Interleukin-1 Beta converting Enzyme
;; Like Apoptosis Protease 3 and 4
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Ave.
;; CITY: Rockville
;; STATE: MD
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/895,263
;; FILING DATE: 02-Jul-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: <Unknown>
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jonathan L. Klein
;; REGISTRATION NUMBER: 41,119
;; REFERENCE/DOCKET NUMBER: PF140
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-251-6015
;; TELEFAX: 301-309-8439
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 303 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-895-263-2

Query Match 2.4%; Score 10; DB 9; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPCLFFQAC 287
| | | | | | | | | |
DB 177 KPCLFFQAC 186

RESULT 29
US-09-944-851-2
;; Sequence 2, Application US/09944851
;; Patent No. US20020102648A1
;; GENERAL INFORMATION:
;; APPLICANT: Alnemri, Emad S.
;; Fernandes-Alnemri, Teresa
;; Litwack, Gerald
;; Armstrong, Robert
;; Tomaselli, Kevin
;; TITLE OF INVENTION: Mch3, A No. US20020102648A1e1 Apoptotic Protease,
;; Nucleic Acids Encoding and Methods of Use
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell and Flores
;; STREET: 4370 La Colla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/944,851
;; FILING DATE: 31-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/556,627
;; FILING DATE: 13-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-ID 1813
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 303 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-851-2

Query Match 2.4%; Score 10; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFQAC 287
| | | | | | | | | |
DB 177 KPCLFFQAC 186

RESULT 30
US-09-954-697-24
;; Sequence 24, Application US/09954697
;; Patent No. US20020106631A1
;; GENERAL INFORMATION:
;; APPLICANT: Alnemri, Emad S.
;; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
;; THEREOF

; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-697-24

Query Match 2.4%; Score 10; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | | | |
DB 177 KPCLFFFIQAC 186

RESULT 31
US-09-851-873-100
; Sequence 100, Application US/99851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Welland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-100

Query Match 2.4%; Score 10; DB 12; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | | | |
DB 177 KPCLFFFIQAC 186

RESULT 32
US-10-280-670-4
; Sequence 4, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-4

Query Match 2.4%; Score 10; DB 12; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | | | |
DB 177 KPCLFFFIQAC 186

RESULT 33
US-10-337-060-2
; Sequence 2, Application US/10337060
; Publication No. US20030119169A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH3, A NOVEL APOPTOTIC PROTEASE.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; FILE REFERENCE: 480140.423D2
; CURRENT APPLICATION NUMBER: US/10/337,060
; CURRENT FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-060-2

Query Match 2.4%; Score 10; DB 15; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | | | |
DB 177 KPCLFFFIQAC 186

RESULT 34
US-10-280-670-2
; Sequence 2, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-2

Query Match 2.4%; Score 10; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | | | |
DB 259 KPCLFFFIQAC 268

RESULT 35

```

US-10-280-670-3
; Sequence 3, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670 3

Query Match      2.4% Score 10; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      278 KPKLFFFIQAC 287
Db      259 KPKLFFFIQAC 268
|||||

RESULT 36
US-09-952-768-2
; Sequence 2, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APO 1 TIC PROTEASE,
; NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Ver. on #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christensen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

```

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-952-768-2

Query Match      2.4% Score 10; DB 9; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      278 KPKLFFFIQAC 287
Db      349 KPKLFFFIQAC 358
|||||

RESULT 37
US-09-954-697-33
; Sequence 33, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-33

Query Match      2.4% Score 10; DB 10; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      278 KPKLFFFIQAC 287
Db      349 KPKLFFFIQAC 358
|||||

RESULT 38
US-09-009-893-4
; Sequence 4, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: I-FLICE, A NOVEL INHIBITOR OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR-1 AND CD-95 INDUCED APOPTOSIS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 60/054,800
FILING DATE: 05-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0970002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-009-893-4

Query Match 2.4%; Score 10; DB 11; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287
| | | | |
Db 349 KPKLFFFIQAC 358
| | | | |

RESULT 39

US-09-962-834A-2
Sequence 2, Application US/09962834A
Patent No. US20020034813A1
GENERAL INFORMATION:
APPLICANT: Bowman, Michael
TITLE OF INVENTION: NOVEL PROTEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,834A
FILING DATE: 25-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,123
FILING DATE: 1996-07-03
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2

Query Match 2.4%; Score 10; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.75;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 278 KPKLFFFIQAC 287
| | | | |
Db 392 KPKLFFFIQAC 401
| | | | |

RESULT 40

US-09-851-873-103
Sequence 103, Application US/09851873
Publication No. US20030165488A1
GENERAL INFORMATION:
APPLICANT: Kietzien, Rolf F
APPLICANT: Reardon, Ilene M
APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851,873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 103
LENGTH: 521
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-103

Query Match 2.4%; Score 10; DB 12; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287
| | | | |
Db 392 KPKLFFFIQAC 401
| | | | |

RESULT 41

US-10-439-676-2
Sequence 2, Application US/10439676
Publication No. US20030180935A1
GENERAL INFORMATION:
APPLICANT: Bowman, Michael
TITLE OF INVENTION: NOVEL PROTEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,676
FILING DATE: 16-May-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/675,123
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids

;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-439-676-2

Query Match 2.4%; Score 10; DB 12; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFIQAC 287
Db 392 KPKLFFIQAC 401

RESULT 42

US-09-410-194-21
; Sequence 21, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Techopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.;
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; JS-09-410-194-21

Query Match 2.4%; Score 10; DB 12; Length 571;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFIQAC 287
Db 392 KPKLFFIQAC 401

RESULT 43

JS-09-954-697-56
; Sequence 56, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPA: S AND USSSES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 9

;
; TYPE: PRT
; ORGANISM: Homo eapien
; US-09-954-697-56

Query Match 2.2%; Score 9; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 FIOACGGEQ 291
Db 1 FIOACGGEQ 9

RESULT 44

US-10-059-749-19
; Sequence 19, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 218C
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-059-749-19

Query Match 2.2%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 FIOACGGEQ 291
Db 1 FIOACGGEQ 9

RESULT 45

US-09-410-194-12
; Sequence 12, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:

```

; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imbler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-410-194-12

```

```

Query Match      2.2% Score 9; DB 9; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      277 GKPKLFFIQ 285
        |||||
DB      352 GKPKLFFIQ 360

```

```

RESULT 46
US-09-410-194-19
; Sequence 19, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Imbler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-410-194-19

```

```

Query Match      2.2% Score 9; DB 9; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      277 GKPKLFFIQ 285
        |||||
DB      352 GKPKLFFIQ 360

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RESULT 47
US-10-005-921-2
; Sequence 2, Application US/10005921
; Publication No. US20020174450A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Leviten, Michael W.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE
; TITLE OF INVENTION: DISRUPTIONS
; FILE REFERENCE: R-714
; CURRENT APPLICATION NUMBER: US/10/005,921
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/254,902
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-005-921-2

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Query Match      2.2% Score 9; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      277 GKPKLFFIQ 285
        |||||
DB      355 GKPKLFFIQ 363

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RESULT 48
US-09-823-394-2
; Sequence 2, Application US/09823394
; Publication No. US20030041344A1
; GENERAL INFORMATION:
; APPLICANT: Chory, Joanne
; APPLICANT: Jianming, Li
; TITLE OF INVENTION: Salk Institute for Biological Studies
; TITLE OF INVENTION: RECEPTOR KINASE, BIN 1
; FILE REFERENCE: SALKINS.012CP1
; CURRENT APPLICATION NUMBER: US/09/823,394
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 08/881,706
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Arabidopsis
US-09-823-394-2

```

```

Query Match      2.2% Score 9; DB 11; Length 1196;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      131 IGSQGFQDV 139
        |||||
DB      889 IGSQGFQDV 897

```

```

RESULT 49
US-10-080-170-242
; Sequence 242, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:

```

```

; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080.170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270.123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 242
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-242

```

```

Query Match 1.9% Score 8; DB 16; Length 579;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 176 GLRTRTGS 183
Db 17 GLRTRTGS 24

```

```

RESULT 50
US-09-965-967-12
; Sequence 12, Application US/09965967
; Patent No. US20020177557A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apopt sis
; FILE REFERENCE: PJ-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965.967
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/236.574
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/256.830
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-967-12

```

```

Query Match 1.7% Score 7; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 316 ATPFQEG 322
Db 1 ATPFQEG 7

```

```

Search completed: October 20, 2003, 12:37:03
Job time : 70 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 20, 2003, 12:07:56 ; Search time 97 Seconds
(without alignments)

1106.700 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKQPGCFNLRKLFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1647	75.6	454	11 Q8C3Q9	Q8C3Q9 mus musculus
2	1645	75.5	454	11 Q9JHK1	Q9JHK1 rattus norv
3	1645	75.5	454	11 Q9ROT0	Q9ROT0 mus musculus
4	1642	75.3	453	11 Q8C3Q0	Q8C3Q0 mus musculus
5	1336	61.3	393	11 Q9ROS9	Q9ROS9 mus musculus
6	1093	50.1	383	11 Q9NM88	Q9NM88 rattus norv
7	1048.5	48.1	399	13 Q9IB63	Q9IB63 xenopus lae
8	1000.5	45.9	403	13 Q90WU0	Q90WU0 gallus gall
9	485	22.2	177	11 Q920G4	Q920G4 rattus norv
10	449	20.6	426	5 Q816Y2	Q816Y2 geodia cydo
11	443	20.3	423	13 Q9IB67	Q9IB67 xenopus lae
12	437	20.0	313	11 Q8CHV5	Q8CHV5 mus musculus
13	435	20.0	316	5 Q817B0	Q817B0 geodia cydo
14	424	19.4	482	11 Q9JHX4	Q9JHX4 rattus norv
15	421	19.3	328	5 Q81TP3	Q81TP3 branchiosto
16	420	19.3	277	6 Q95ND5	Q95ND5 sus scrofa

17	419	19.2	277	6 Q8MJU1	Q8MJU1 felis ailve
18	418	19.2	280	13 Q8JGM9	Q8JGM9 fugu rubrip
19	414	19.0	452	11 Q55194	Q55194 rattus norv
20	413	18.9	280	13 Q8JG42	Q8JG42 fugu rubrip
21	411	18.9	452	11 Q8K241	Q8K241 mus musculus
22	410	18.8	452	11 Q8C9H7	Q8C9H7 mus musculus
23	406	18.6	435	4 Q9BUP7	Q9BUP7 homo sapien
24	402.5	18.5	318	13 Q9IB65	Q9IB65 xenopus lae
25	401	18.4	277	6 Q8MKI5	Q8MKI5 canis famil
26	401	18.4	277	6 Q8MJC3	Q8MJC3 oryctolagus
27	396	18.2	283	13 Q93417	Q93417 gallus gall
28	393	18.0	282	13 Q98UI8	Q98UI8 brachydanio
29	387.5	17.8	482	13 Q90WU1	Q90WU1 gallus gall
30	384	17.6	280	13 Q8JIS9	Q8JIS9 oryzias lat
31	383.5	17.6	476	13 Q9IBJ3	Q9IBJ3 brachydanio
32	378.5	17.4	290	13 Q8JIS8	Q8JIS8 oryzias lat
33	363	16.7	220	11 Q9QW14	Q9QW14 mus musculus
34	362.5	16.6	303	11 Q88550	Q88550 rattus norv
35	362	16.6	182	6 Q77623	Q77623 ovis aries
36	355	16.3	479	4 Q8WYQ8	Q8WYQ8 homo sapien
37	344.5	15.8	522	4 Q81UP5	Q81UP5 homo sapien
38	330.5	15.2	400	5 Q81TP2	Q81TP2 branchiosto
39	330	15.1	417	5 Q9YIU6	Q9YIU6 pristiionchu
40	326.5	15.0	304	13 Q93415	Q93415 gallus gall
41	322	14.8	276	11 Q99M47	Q99M47 mus musculus
42	321	14.7	276	11 Q9D089	Q9D089 mus musculus
43	318	14.6	520	13 Q9IB62	Q9IB62 xenopus lae
44	314	14.4	303	13 Q9IB66	Q9IB66 xenopus lae
45	312	14.3	189	11 Q8BNT4	Q8BNT4 mus musculus

ALIGNMENTS

RESULT 1

Q8C3Q9 ID Q8C3Q9 PRELIMINARY; PRT; 454 AA.
AC Q8C3Q9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Caspase 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK085095; BAC39365.1; ..
SQ SEQUENCE 454 AA; 49979 MW; 438A67EA66A6EE78 CRC64;

Query Match 75.6%; Score 1647; DB 11; Length 454;
Best Local Similarity 71.6%; Pred. No. 8.4e-140;
Matches 325; Conservative 28; Mismatches 63; Indels 38; Gaps 2;
QY 1 MDEADRLRLRCRLRLVEELQVDLWDVLLSLRFLPHMIEDIQRAGSGRRDQARQLII 60
DB 1 MDEARQLRLRCRLRLVEELQVDLWDVLLSLRFLPHMIEDIQRAGSGRRDQARQLV 60
QY 61 DLETRGQALPLFISCLETDGQDMLASFLRTNRQAGL----- 98
DB 61 DLETRGQALPLFISCLETDGQDMLASFLRTNRQAGL----- 98
QY 99 -----SKPTLENLTPVVLRLPE-----IRPEVLRLPTPRPVDIGSGGFGDVGAL 142
DB 121 AEQRVYKLPQSPQAVGNLTPVVLGPEELPARLRLPEVLRPVDIGSGGAGHDCVP 180


```
143 ESURGNADLAYILSMPCGCHLIINNVPFCRESG RTRTGSNIDCEKLRFRFSSLHFVME 202
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 GKIRGHADMAVTLDSDCGCHLIINNVPFCPSG RTRTGSNLDKLEHFRWLRFMVME 240
HSSP: P42574; 1PAU.
203 VKGDLTAKKVVALLLELARDHGDGCVVILSHG: QASHLQFPGAVYGTDCGVSVEK 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 VKNDLTAKKVVALLLELARDHGDGCVVILSHG: QASHLQFPGAVYGTDCGVSVEK 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
263 IVNIENGTCSPSLGCKPKLFFIQACGCEQKHGFEVASTSPEDSGSNPEPDATPFQEG 322
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 IVNIENGTCSPSLGCKPKLFFIQACGCEQKHGFEVASTSPEDSGSNPEPDATPFQEG 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
323 LRTFDQDLAISLPTSDIFVSYSTFPFGVSWRDKSGSWYVETLDDIFQWHAHSEDLOS 382
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
361 PRPLDQDQVAYSSLPTSDIFVSYSTFPFGVSWRDKSGSWYVETLDDIFQWHAHSEDLOS 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
383 LLRLVANAVSVKGIYKOMPCCGFNLRKKLFKTS 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
421 LLRLVANAVSAKGIYKQIPGCFNLRKKLFKTS 454
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
9JHK1
D Q9JHK1 PRELIMINARY; PRT; 454 AA
C Q9JHK1
T 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E Caspase-9 (Caspase-9 long isoform).
N RNCASP9.
S Rattus norvegicus (Rat).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
X NCBI_TaxID=10116;
N SEQUENCE FROM N.A.
P STRAIN=SPRAGUE-DAWLEY;
A Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;
"Cloning and Characterization of Rat Caspase-9: Implication for a Role
in Neuronal Cell Death During Brain Development and Transient Cerebral
Ischemia.";
L Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
N [2]
P SEQUENCE FROM N.A.
C STRAIN=SPRAGUE-DAWLEY;
A Itoh T., Itoh A., Pleasure D.;
Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
L [3]
P SEQUENCE FROM N.A.
C STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
A Cao G., Chen D., Graham S., Simon R.P., Ch. J.;
"Cloning and Characterization of Rat Caspa 9: Implication for a Role
in Neuronal Cell Death During Brain Development and Transient Cerebral
Ischemia.";
L Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
N [4]
P SEQUENCE FROM N.A.
MEDLINE=2119275; PubMed=11278518;
A Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
Frankie T.F.;
"Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
Apoptosis.";
L J. Biol. Chem. 276:12190-12200(2001).
N [5]
P SEQUENCE FROM N.A.
C STRAIN=WKY;
A MEDLINE=21552893; PubMed=11695991;
A Nishiyama J., Yi X., Venkatachalam M.A., D. J.;
"CDNA cloning and promoter analysis of rat Caspase-9.";
L Biochem. J. 360:49-56(2001).
R EMBL; AF262319; AAF85658.1; -.
R EMBL; AF271996; AAF76217.1; -.
R
```

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DR EMBL; AF286006; AAF99705.1; -.
DR EMBL; AF308469; AAK35159.1; -.
DR EMBL; AY027667; AAK26235.1; -.
DR HSSP: P42574; 1PAU.
DR MEROPS; C14.010; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0122; CASPASE_CYS; 1.
DR PROSITE; PS0121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0207; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50399 MW; 501623B29E6ED6FC CRC64;

Query Match 75.5%; Score 1645; DB 11; Length 454;
Best Local Similarity 71.1%; Pred. No. 1.3e-139;
Matches 323; Conservative 32; Mismatches 61; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDQLVLLSRELPRPHMIEDIQAGSGRRDQARQLII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDEADQLRLRCRLRLVEELQVDQLVLLSRELPRPHMIEDIQAGSGRRDQARQLVI 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DLETRGSOALPLFISCLEETGQDMLASFLRTNRQAGL----- 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DLETRGSOALPRFISCLEETGQGSLSFLQSSGAAKQDPEAVTPLDHLVPLVPLGPMGLK 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 99 -----SKPTLENLTPVLRPE-----IRKEVLRLPETPRPVDIGSGGFDVGAL 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 SKEQKVVLKDPSPALGNLTPVLRPELWTRLRPELTPETPRPVDIGSGRAHDVCTP 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 143 ESLRGADLAYILSMPCGCHLIINNVPFCRESGLRTRTGSNIDCEKLRFRFSSLHFVME 202
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 GKIERHADMAVTLDSDCGCHLIINNVPFCPSGSLTRIGSHVDCCKLQHRFCMLRPMVE 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 203 VKGDLTAKKVVALLLELARDHGDGCVVILSHGCOASHLQFPGAVYGTDCGVSVEK 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 VKNDLTAKKVVALLLELARDHGDGCVVILSHGCOASHLQFPGAVYGTDCGVSVEK 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 263 IVNIENGTCSPSLGCKPKLFFIQACGCEQKHGFEVASTSPEDSGSNPEPDATPFQEG 322
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 IVNIENGTCSPSLGCKPKLFFIQACGCEQKHGFEVASTSPEDSGSNPEPDATPFQEG 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 323 LRTFDQDLAISLPTSDIFVSYSTFPFGVSWRDKSGSWYVETLDDIFQWHAHSEDLOS 382
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 PRPLDQDQVAYSSLPTSDIFVSYSTFPFGVSWRDKSGSWYVETLDDIFQWHAHSEDLOS 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 383 LLRLVANAVSVKGIYKOMPCCGFNLRKKLFKTS 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 LLRLVANAVSEKGIYKQIPGCFNLRKKLFKTS 454
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Q9ROT0
ID Q9ROT0 PRELIMINARY; PRT; 454 AA.
AC Q9ROT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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```

P SEQUENCE FROM N.A.
X MEDLINE=20001956; PubMed=10529400;
A Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
T "Akt phosphorylation site found in human caspase-9 is absent in mouse
T caspase-9.";
T Biochem. Biophys. Res. Commun. 264:550-555(1999).
L EMBL: AB019600; BAA86895.1; -
R HSP: P42574; 1PAU.
R MEROPS: C14.010; -.
R MGD; MGI:127950; Casp9.
R InterPro; IPR001315; CARD.
R InterPro; IPR002398; ICE.
R InterPro; IPR002138; ICE_p10.
R InterPro; IPR001309; ICE_p20.
R Pfam; PF00619; CARD; 1.
R Pfam; PF00655; ICE_p10; 1.
R Pfam; PF00656; ICE_p20; 1.
R PRINTS; PR00376; I1BICENZYME.
R SMART; SM00114; CARD; 1.
R SMART; SM00115; CASC; 1.
R PROSITE; PS02029; CARD; 1.
R PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PSS0207; CASPASE_P10; 1.
R PROSITE; PSS0208; CASPASE_P20; 1.
Q SEQUENCE 454 AA; 50051 MW; 4614989AF823850F CRC64;

Query Match 75.5%; Score 1645; DB 11; Length 454;
Best Local Similarity 71.6%; Pred. No. 1.3e-139;
Matches 325; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

Y 1 MDEADRLRLRCRLRLVEELQVQDLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
b 1 MDEADRLRLRCRLRLVSELQVAELWDALLSRELFRTRDMIEDIQAGSGRRDQARQLVT 60
y 61 LETRGSOALPLFISCLDGTGQDMLASFRTNRQAGKL ----- 98
b 61 LETRGSOALPLFISCLDGTGQTLASLQSGRQAQKQDPEAVKPLDHLVPVVLGPMGLT 120
y 99 -----SKTLENLTPVVLPE-----IRKPEVLRLPETPRPVDIGSGGFGVGALE 142
b 121 KEQVRVKLPSPQAVGNLTPVVLPEELWPARKPEVLRLPETPRPVDIGSGGAGHVCVP 180
y 143 ESLRGADLAYILSMPCGCHLIINNVCRESGLTRTGSNIDCEKLRFRFSLHFMWE 202
b 181 KIRGHADMAITLDSDFCGHCLIIINNVCPSGLGTRTGSNLDRLDKLEHFRFLRMFVE 240
y 203 VKGDLTAKKMWLALLELARODHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGVSVEK 262
b 241 VKNLTAKKMWLTALMEAHNRHRLDCCFVVVILSHGCOASHLQFPGAVYGTDCGVSVEK 300
y 263 IVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGEVASTSPEDSPGNPEPATPFQEG 322
b 301 IVNIFNGSGCPSLGGKPKLFFIQACGGEQKDHGEVACTSSQGRITLDSSEPDAPVYQEG 360
y 323 LRTFDQLDAISSLPTSDIFVSYSTFGFVSWRDKKSGSWYVETLDDIFEQWHSDELQS 382
b 361 PRPLDQLDAVSSLPTSDILVSYSTFGFVSWRDKKSGSWYIETLDGILEQWARSDELQS 420
y 383 LLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
b 421 LLRVANAVSEKGYKQIPGCFNLRKLLFFKTS 154

RESULT 4
8C300 PRELIMINARY; PRT; 453 AA.
C 08C300;
T 01-MAR-2003 (TrEMBLrel. 23, Created)
T 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
E Caspase 9 (Fragment).
S Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RL Nature 420:563-573(2002).
DR EMBL; AK085152; BAC33378.1; -.
FT NON_TER 1
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA68F CRC64;

Query Match 75.3%; Score 1642; DB 11; Length 453;
Best Local Similarity 71.5%; Pred. No. 2.4e-139;
Matches 324; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

QY 2 DEADRLRLRCRLRLVEELQVQDLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLIID 61
DB 1 DEADRLRLRCRLRLVSELQVAELWDALLSRELFRTRDMIEDIQAGSGRRDQARQLVTD 60
QY 62 LETRGSOALPLFISCLDGTGQDMLASFRTNRQAGKL ----- 98
DB 61 LETRGSOALPLFISCLDGTGQTLASLQSGRQAQKQDPEAVKPLDHLVPVVLGPMGLTA 120
QY 99 -----SKTLENLTPVVI:PE-----IRKPEVLRLPETPRPVDIGSGGFGVGALE 143
DB 121 KEQVRVKLPSPQAVGNLTPVVL:PEELWPARKPEVLRLPETPRPVDIGSGGAGHVCVP 180
QY 144 SURGNADLAYILSMPCGCHLIINNVCRESGLTRTGSNIDCEKLRFRFSLHFMVEV 203
DB 181 KIRGHADMAITLDSDFCGHCLIIINNVCPSGLGTRTGSNLDRLDKLEHFRFLRMFVEV 240
QY 204 KGDLTAKKMWLALLELARODHGALDCCVVVILSHGCOASHLQFPGAVYGTDCGCPVSVKEI 263
DB 241 KNDLTAKKMWLTALMEAHNRHRLDCCFVVVILSHGCOASHLQFPGAVYGTDCGCVSIEKI 300
QY 264 VNI FNGTSCPSLGGKPKLFFIQACGGEQKDHGEVASTSPEDSPGNPEPATPFQSGL 323
DB 301 VNI FNGSGCPSLGGKPKLFFIQACGGEQKDHGEVACTSSQGRITLDSSEPDAPVYQEG 360
QY 324 RTFDQLDAISSLPTSDIFVSYSTFGFVSWRDKKSGSWYVETLDDIFEQWHSDELQSL 383
DB 361 RPLDQLDAVSSLPTSDILVSYSTFGFVSWRDKKSGSWYIETLDGILEQWARSDELQSL 420
QY 384 LLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
DB 421 LLRVANAVSAKTYKQIPGCFNLRKLLFFKTS 453

RESULT 5
Q9ROS9 PRELIMINARY; PRT; 393 AA.
AC Q9ROS9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Caspase9S.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
RT caspase-9.";
RT Biochem. Biophys. Res. Commun. 264:550-555(1999).
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).

```

EMBL; AB019601; BAA86896.1; --
HSP; P42574; 1PAU.
MEROPS; C14.010; --
MGD; MG1.1277950; Casp9.
InterPro; IPR001315; CARD.
InterPro; IPR002398; ICE.
InterPro; IPR001309; ICE_p20.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS02029; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02028; CASPASE_P20; 1.
SEQUENCE 393 AA; 42975 MW; CA889475E50DD632 CRC64;
Query Match 61.3%; Score 1336; DB 11; Length 393;
Best Local Similarity 68.8%; Pred. No. 7.4e-112;
Matches 267; Conservative 26; Mismatches 57; Indels 38; Gaps 2;
1 MDEADRLRLRLVEELQVDQLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLII 60
1 MDEADRLRLRLVEELQVDQLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLVT 60
61 DLETRGQALPLFISCLEDTGQDMLASFLRTNRQAGL.. 98
61 DLETRGQALPLFISCLEDTGQDMLASFLRTNRQAGL.. 120
99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRLPETPRPVDIGSGFGDVGAL 142
121 AKQRVVKLPSQAVGNLTPVVLGPELWPAR..PEVLRLPETPRPVDIGSGAHDVCP 180
143 ESLRGNADLAYILSMPCGHCLIIINNVPFCRESGLRTGNSIDCEKLRFRFSLHFMVE 202
181 GKIRGHADMAYTLDSDFCGHCLIIINNVPFCPSGLGTRTGSNLDKRLKHLRFRWLFMVE 240
203 VKGDLTAKKMWLALLELARQDHGALDCVVVILSHGCOASHLOFPQAVYGTDCGCVSVEX 262
241 VKNDLTAKKMYTALMEMAHRHRLDCFVVVILSHGCOASHLOFPQAVYGTDCGCVSIEK 300
263 IVNIFNGTSCPSLGKPKLFFIOACGGEQKHGFEVASTSPEDSPSNPEPDATPFQEG 322
301 IVNIFNGSGCPSLGKPKLFFIOACGGEQKHGFEVASTSQORTLDSSEPDVAVPYQEG 360
323 LRTFDQLCAISSLTPSDIFVSYSTFPG 350
361 PRPIQDLDAVSSLTPSDILVSYSTFPG 398
RESULT 6 99M88
Q99M88 PRELIMINARY; PRT; 383 AA.
Q99M88: C
01-JUN-2001 (Tremblrel. 17, Created)
01-JUN-2001 (Tremblrel. 17, Last sequence update)
01-MAR-2002 (Tremblrel. 20, Last annotation update)
Caspase-9 CTD isoform.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
MEDLINE=21192275; PubMed=11278518;
Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
Frank T.F.,
"Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
Apoptosis";
J. Biol. Chem. 276:12190-12200(2001).
EMBL; AY008275; AAG21690.1; --
HSP; P42574; 1PAU.

DR MEROPS; C14.010; --
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
SQ SEQUENCE 383 AA; 42319 MW; 3C5D217C3100FF25 CRC64;
Query Match 50.1%; Score 1093; DB 11; Length 383;
Best Local Similarity 67.3%; Pred. No. 5.6e-90;
Matches 220; Conservative 22; Mismatches 47; Indels 38; Gaps 2;
CY ; MDEADRLRLRLVEELQVDQLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRLVEELQVDQLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLVI 60
QY 61 DLETRGQALPLFISCLEDTGQDMLASFLRTNRQAGL.. 98
Db 61 DLETRGQALPLFISCLEDTGQDMLASFLRTNRQAGL.. 120
QY 99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRLPETPRPVDIGSGFGDVGAL 142
Db 121 SKEQVVKLPSQAVGNLTPVVLGPELWPAR..PEVLRLPETPRPVDIGSGAHDVCTP 180
QY 143 ESLRGNADLAYILSMPCGHCLIIINNVPFCRESGLRTGNSIDCEKLRFRFSLHFMVE 202
Db 181 GKIERHADMAYTLDSDFCGHCLIIINNVPFCPSGLSTRIGSHVDCEKLRFCWLFMVE 240
QY 203 VKGDLTAKKMWLALLELARQDHGALDCVVVILSHGCOASHLOFPQAVYGTDCGCVSVEX 262
Db 241 VKNDLTAKKMYTALMEMAHRHRLDCFVVVILSHGCOASHLOFPQAVYGTDCGCVSVIER 300
QY 263 IVNIFNGTSCPSLGKPKLFFIOACGG 289
Db 301 IVNIFNGTSCPSLGKPKLFFIOACGG 327
RESULT 7
Q91B63
Q91B63 PRELIMINARY; PRT; 399 AA.
AC Q91B63
ID Q91B63
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20209426; PubMed=10744739;
RX Nakajima K., Takahashi A., Yaoita Y.,
RA "Structure, expression and function of the Xenopus laevis caspase
RT family";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; --
DR HSP; Q15806; 1QDU.
DR MEROPS; C14.010; --
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

[illegible]

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RESULT 12
Q8CHV5 PRELIMINARY; PRT; 313 AA.
Q8CHV5:
01-MAR-2003 (Tremblrel. 23, Created)
01-MAR-2003 (Tremblrel. 23, Last sequence update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
Caspase 3, apoptosis related cysteine protease (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Odontia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=FVB/N;
Strauberg R.;
Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
EMBL: BC038825; AAB38825.1; -.
Protease.
NON_TER.
SEQUENCE 313 AA; 35174 MW; 96E98A1F04E763 7 CRC64;

Query Match 20.0%; Score 437; DB 11; Length 313;
Best Local Similarity 31.5%; Pred. No. 5,6e-31;
Matches 106; Conservative 52; Mismatches 123; Indels 56; Gaps 5;

87 SFLRTNQAGKLSKPTLENLTPVVLRLPEIRKPEVLRPETPRPVDIGSGGFGDVGALSSLR 146
21 SVLRGAWNGTLRKVTWENNNTSVDSKINNFEVKTTHGSKSVDSGI----- 67
147 GNADLAYILSMPCGHCLINNFCRESGLTRTGSNIDCEKLRFRFSSLHFHVEVKGD 206
68 -YLDSSVNDYDPEMGCICIIINNKPHKSTGSSRGTDVDAANLRETFMGUKYQVRNKD 126
207 LTAKKMLALLELARQHGALDCCVVVILSHGCOASHLQFPAGVYGTDCGCPVSVEKIVNI 266
127 LTREDILEMDSVSKEDHSSKSSFCVILSHGDE-----GVYINGT-PVELKKLTSP 178
267 FNGTSCPSLGKPKLFFTOACGGQKHGFRVASTSPEDSGNSPEPNPDATPFOEGLRTF 326
179 FRGDCRLTGKPKLFFIOACRGTELDGCIETDGTDEM----- 218
327 DQDAISLTPSDIFVSYSTFRGFSWRDPKSGSWYVETLDDIFEQWASEDLQSLLR 386
219 ----ACQIPVEADFLYATSTAGPYSWRNSEYGSWFIKAFVDTMRDLASKEHFMDILTEVNRKVAYDFQ 274
387 VANAVSVK-----GIYKQMPGCCFNFLRKKLFF 413
275 VNRKVATEFESFLDSTPHAKQIPCIIVSLTKE. 311

PRELIMINARY; PRT; 316 AA.
Q817B0:
01-MAR-2003 (Tremblrel. 23, Created)
01-MAR-2003 (Tremblrel. 23, Last sequence update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
Caspase 3.
Geodia cydonium (sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Astrophorida; Geodiidae; Geodia.
NCBI_TaxID=6047;
[1]
SEQUENCE FROM N.A.
Wiens M., Saenger H., Krasko A., Perovic S., Mueller M.E.G.;
"Caspase-mediated apoptosis in sponges: cloning and function.";
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AJ417903; CAD10676.1; -.
SEQUENCE 316 AA; 35319 MW; 33A46BCCE6C3F9B7 CRC64;

Query Match 20.0%; Score 435; DB 5; Length 316;
Best Local Similarity 35.1%; Pred. No. 8,7e-31;
Matches 113; Conservative 44; Mismatches 121; Indels 44; Gaps 9;

QY 111 LRPEIRKPEVLRPETPRPVDIGSGGFGDVGALSSLRGNADLAYILSMPCGHCLINN 170
DB 10 VRPLIAPTATSHPPPIPPPEEGT---DAGRKD-----AYKMSRRPRGMALIINRN 57
QY 171 FCRESGLTRTGSNIDCEKLRFRFSSLHFHVEVKGDLTAKKMLALLELARQHGALDCC 230
DB 58 F--TCGMKERVGTGDAENLYGLFNWLGMATIRKDLTGKAMTRFEDLARRDHSAYDCV 115
QY 231 VVILSHGCOASHLQFPAGVYGTDCGCPVSVEKIVNIFNGTSCPSLGKPKLFFIQACGGE 290
DB 116 VVALTHG-----ISGRLYSTDGDLIPVEDITKYFDGVRNPSLIGKPKVFFVQACRG 168
QY 291 QKHGFEVASTSPEDSGNSPEPNPDATPFOEGLRTFDQ-----LDA-----ISSLP 336
DB 169 KFDYGVSESTDCGESVN--KETANEMME--KQFDKVVVEKALDADETGGGYSREALP 223
QY 337 TPSDIFVSYSTFRGFSWRDPKSGSWYVETLDDIFEQWASEDLQSLLRVANAVSV--- 393
DB 224 TEADFVLAYATVPGYSWRNSEYGSWFIKAFVDTMRDLASKEHFMDILTEVNRKVAYDFQ 283
QY 394 -GIYKQMPGCCFNFLRKKLFFK 414
DB 284 SRGNKQIPAPVTMLTRKLYFR 305

PRELIMINARY; PRT; 482 AA.
Q9JHX4:
AC Q9JHX4 PRELIMINARY; PRT; 482 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Caspase-8.
GN CASP8
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Itoh T., Itoh A., Pleasure D.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
PP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Graham S.H., Chen D., Chen J.;
RT "Molecular cloning and characterization of rat caspase-8: Its
RT implication in delayed neuronal cell death after ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279308; AAF87778.1; -.
DR EMBL: AF288372; AAK83055.1; -.
DR HSP: Q15806; IQDU.
DR MEROPS: C14.009; -.
DR InterPro: IPR001875; DED.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF01335; DED; 2.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; IL1BENZVME.
DR SMART: SM00115; CASc; 1.
DR SMART: SM00031; DED; 2.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS50168; DED; 2.
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SEQUENCE	482 AA; 55339 MW; 82B4A29330C53264 CRC64;	
Query Match	19.4%; Score 424; DB 11; Length 482;	
Best Local Similarity	29.9%; Pred. No. 1.5e-29;	
Matches	138; Conservative 60; Mismatches 173; Indels 90; Gaps 14;	
15	RVTEE--LQVQLQDMDVLSRELPRPHMIEDIQAGSGRRDQARQLIIDLETRGSQALPL 72	
47	RLOEGMLEEDNL--SFLKELLFHISRRLDLLSRVLKSSPEEMVRELOVLGKAQVSAYRVM 104	
73	FISCLEDTGDOMLASF---LRTRQAGKLSKPTLENLTPVVLRLPEIRKPEVL----- 121	
105	LFKLSEDMOKEDLKSFKELLITETPKCKLQ---DNSLLDIFVEMEKRTILAENNLVTL 160	
122	-----RPETPRPVDIGSGG-----FGDVGALLES 145	
161	KSICFRVNRSLGRIDDYERSSTERRMSTEGEELPYSVLDEVTIKMQDMWDSFGEQSE 220	
146	RGNADLAYILSMERCGHCLIIINNVF--CRE-----SGLRTRTGSNIDCEKLRFRFSLH 198	
221	SLNSDNVYQMKSKPRGYCLIFNNNFNSKAREDIPKLSNMRDRKGTNYDEEALSKTFKELH 280	
199	PMVEVKDGLTAKKMYLALLELARODHGALDCVVVILSHGCOASHLQFPGAVYGTDCPV 258	
281	PEIYVSFSDCTASQIHEVLVSQSKDHKQKCFICILSHGDK-----GIVYGTGKEA 333	
259	SVEKIVNIFNCTGSCPSLGKPKLFFIQACGGEQKHGFVASTSPEDSPGNSPEPDATP 318	
334	SIYELTSYFTGSKCPSLAGKPKIFFIQACQ---NNFQKAV-----PVPDETG 378	
319	F-OGLRTPFDQDAISSLPSTDIFVSVSTFPFVSVWRDPKSGSWYVETL-DDIFEQWAH 376	
379	LEQEHVLEEDSSSYKNYIPDEADFLGMAIVKNCVS/RDPTRTGMYIQSLCCQSURERCPR 438	
377	SEDLQSL---LRVANAVSVKGIYKOMPCCFNFLK 413	
439	GEDILSLITGVNVDVSNKDNPRNMCKQMPQPIFTLPK 479	
RESULT 15		
Q81TP3	PRELIMINARY; PRT; 328 AA.	
Q81TP3		
Q81TP3		
01-MAR-2003	(TremBLrel. 23, Created)	
01-MAR-2003	(TremBLrel. 23, Last sequence update)	
01-MAR-2003	(TremBLrel. 23, Last annotation update)	
AmphicASP-3/7		
Branchiostoma floridae	(Florida lancelet) (Amphioxus).	
Eukaryota; Metazoa;	Chordata; Cephalochordata; Branchiostomidae;	
Branchiostoma.		
NCBI_TaxID=7739;		
[1]		
SEQUENCE FROM N.A.		
MEDLINE=22217375; PubMed=12232796;		
Bayascas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,		
Comella J.X.;		
*Isolation of AmphicASP-3/7, an ancestral caspase from amphioxus		
(Branchiostoma floridae). Evolutionary considerations for vertebrate		
caspases.*;		
Cell Death Differ. 9:1078-1089(2002).		
EMBL: AF412335; AAN45849.1;		
SEQUENCE 328 AA; 36327 MW; 1D46760AF47184 B CRC64;		
Query Match	19.3%; Score 421; DB 5; Length 328;	
Best Local Similarity	36.4%; Pred. No. 1.7e-29;	
Matches	96; Conservative 41; Mismatches 87; Indels 40; Gaps 6;	
161	GHCILINNVNFRBSGLTRTGSNIDCEKLRFRFSLHFMVEVKDGLTAKKMYLALLELA 220	
87	GOAIIINNKDFEKHTGMNTRGTDLDANNLYRIFSKLGFETKVFDFNLPCRILSVLQAA 146	
221	RODHGALDCCVVVILSHGCOASHLQFPGAVYGTDCPVSVKIVNIFNGTSCPSLGKPK 280	

Db	147	REDHRVDVCFACAILSHGEE-----GVIYGTG-DHMEVTEVTKPFRGDRCPGLVGKPK 198
Qy	281	LFFIQACGGEQKHGFVASTSPEDSPGNSPEPDATPFQEGRLRTFDQLDA--ISSLPTP 338
Db	199	LFFLQACRGNEFDHGVDM-----PDALP-----EVDGLDAGNKATLPAE 238
Qy	339	SDIFVSYSTFPFVSVWRDPKSGSWYVETLDDIFEQWAHSEDLSQSLLRVANAVS----- 392
Db	239	ADFLLAYSTVPGYYSWRNPGRGSWYIQALCAVLREBGTDLQIMQLLRVNKLVAYDFHSN 298
Qy	393	-----VKGIYKOMPCCFNFLK 412
Db	299	SDNPYNNRKKQIIPCIMSLTKDLF 322
Search completed: October 20, 2003, 12:13:27		
Job time : 101 secs		

GenCore version 5.1.6
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OM protein - protein search, using ew model

Run on: October 20, 2003, 12:09:51 : Search time 29 Seconds
(without alignments)
606.942 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKMPGCFNLRKKLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/aaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/2/aaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/2/aaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/2/aaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/2/aaa/PCUS_COMB.pep:*
- 6: /cgn2_6/prodata/2/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2180	100.0	416	3	US-08-852-936C-1
2	2180	100.0	416	3	US-09-300-328-1
3	2180	100.0	416	4	US-09-069-023-23
4	2157	98.9	416	4	US-09-561-756-30
5	2157	98.9	416	4	US-09-227-721-30
6	2153	98.8	416	3	US-09-257-218-2
7	2153	98.8	416	3	US-09-311-760-2
8	2153	98.8	416	4	US-08-865-579-2
9	2153	98.8	416	4	US-10-059-749-2
10	1083	49.7	203	3	US-08-852-936C-4
11	1083	49.7	203	3	US-09-300-328-4
12	418	19.2	277	3	US-08-591-605-2
13	418	19.2	277	3	US-08-964-308-6
14	418	19.2	277	3	US-08-462-969B-4
15	418	19.2	277	3	US-08-964-313-6
16	418	19.2	277	4	US-09-069-138-6
17	418	19.2	277	4	US-09-561-756-12
18	418	19.2	277	4	US-09-227-721-12
19	418	19.2	277	4	US-08-983-502-30
20	418	19.2	277	4	US-09-124-934A-4
21	418	19.2	277	4	US-08-724-378D-5
22	418	19.2	277	4	US-08-334-251D-4
23	418	19.2	277	4	US-09-516-747-30
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25	409	18.8	277	5	US-08-890-542A-2
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27	409	18.8	421	4	US-09-516-747-10

Sequence 10, Appl
Sequence 53, Appl
Sequence 51, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 4, Appl
Sequence 44, Appl
Sequence 43, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 20, Appl
Sequence 5, Appl
Sequence 36, Appl
Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852.936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-852-936C-1

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Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.4e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
DB 1 MDEADRLRLRCRLRLVEELQVDQMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 61 DLETRGSOALPLFLISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSOALPLFLISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESRLGNADLAYILSMPCGCHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRPVDIGSGGFGDVGALESRLGNADLAYILSMPCGCHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
QY 241 ASHLOFPAGVYGTDCGPVSVEKIVNIENGTSCPSLGGKPKLFFIQAACGGGKDHGFEVAS 300
DB 241 ASHLOFPAGVYGTDCGPVSVEKIVNIENGTSCPSLGGKPKLFFIQAACGGGKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSI TSPDIFVSYSYTFPGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSI TSPDIFVSYSYTFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWHAHSEDQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWYVETLDDIFEQWHAHSEDQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

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RESULT 2

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US-09-300-328-1
; Sequence 1, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rainer & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300.328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852.936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018.961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020.344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017.949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23.031
; REFERENCE/DOCKET NUMBER: P50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-300-328-1

Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.4e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 60
QY 61 DLETRGSOALPLFLISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSOALPLFLISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESRLGNADLAYILSMPCGCHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRPVDIGSGGFGDVGALESRLGNADLAYILSMPCGCHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
QY 241 ASHLOFPAGVYGTDCGPVSVEKIVNIENGTSCPSLGGKPKLFFIQAACGGGKDHGFEVAS 300
DB 241 ASHLOFPAGVYGTDCGPVSVEKIVNIENGTSCPSLGGKPKLFFIQAACGGGKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSI TSPDIFVSYSYTFPGFVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSI TSPDIFVSYSYTFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWHAHSEDQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWYVETLDDIFEQWHAHSEDQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 3
US-09-069-023-23
; Sequence 23, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koekei, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069.023A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-23

Query Match      100.0%; Score 2180; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.4e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MDEADRLRLRRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
1 MDEADRLRLRRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
121 LRPETPRPVDIGSGGFGDVGALSLRGADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
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181 TGSNIDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCC 240
181 TGSNIDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCC 240
241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGKPKLFFFIQACGGEQKHGFVEAS 300
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301 TSPEDSGSNPEPDATPFOEGLRTFDQDLSLPTSDIFVSYSTFPFVSWRDPKSG 360
301 TSPEDSGSNPEPDATPFOEGLRTFDQDLSLPTSDIFVSYSTFPFVSWRDPKSG 360
361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
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RESULT 4
US-09-561-756-30
; Sequence 30, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.5e-227;
Matches 412; Conservative 0; Mismatches Indels 0; Gaps 0;

1 MDEADRLRLRRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
1 MDEADRLRLRRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
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241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGKPKLFFFIQACGGEQKHGFVEAS 300
301 TSPEDSGSNPEPDATPFOEGLRTFDQDLSLPTSDIFVSYSTFPFVSWRDPKSG 360
301 TSPEDSGSNPEPDATPFOEGLRTFDQDLSLPTSDIFVSYSTFPFVSWRDPKSG 360
361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416

RESULT 5
US-09-227-721-30
; Sequence 30, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.5e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGLSKPTLENLTTPVLRPEIRKPEV 120
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241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGKPKLFFFIQACGGEQKHGFVEAS 300
301 TSPEDSGSNPEPDATPFOEGLRTFDQDLSLPTSDIFVSYSTFPFVSWRDPKSG 360
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361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416
361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPFCNFKLFFKTS 416

RESULT 6
US-09-257-218-2
; Sequence 2, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 7
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/257,218
CLASSIFICATION:
PRIORITY APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-257-218-2

Query Match 98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MDEADRLRLRRLVEELQVDLWDLVLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRRLVEELQVDLWDLVLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETGSOALPLFISCLDTGDMLASFLTRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
Db 61 DLETGSOALPLFISCLDTGDMLASFLTRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
Qy 121 LRPEPRPVVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPEPRPVVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Qy 181 TGSNDCEKLRFRFSSHPFVMEVKGDLTAKVMVLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNDCEKLRFRFSSHPFVMEVKGDLTAKVMVLALLELARQDHGALDCCVVVILSHGQ 240
Qy 241 ASHLOFPGAVYTGDCPVSVVEKIVNIFNGTSCPSLGKPKLFFIACGGEQKDHGEVAS 300
Db 241 ASHLOFPGAVYTGDCPVSVVEKIVNIFNGTSCPSLGKPKLFFIACGGEQKDHGEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTPTPSDIFVSYSTFPFVSMRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTPTPSDIFVSYSTFPFVSMRDPKSG 360
Qy 361 SWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 7

US-09 311-760-2
; Sequence 2. Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/311,760
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION NUMBER: 08/865,579
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-311-760-2

Query Match 98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MDEADRLRLRRLVEELQVDLWDLVLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRRLVEELQVDLWDLVLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETGSOALPLFISCLDTGDMLASFLTRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
Db 61 DLETGSOALPLFISCLDTGDMLASFLTRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
Qy 121 LRPEPRPVVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPEPRPVVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Qy 181 TGSNDCEKLRFRFSSHPFVMEVKGDLTAKVMVLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNDCEKLRFRFSSHPFVMEVKGDLTAKVMVLALLELARQDHGALDCCVVVILSHGQ 240
Qy 241 ASHLOFPGAVYTGDCPVSVVEKIVNIFNGTSCPSLGKPKLFFIACGGEQKDHGEVAS 300
Db 241 ASHLOFPGAVYTGDCPVSVVEKIVNIFNGTSCPSLGKPKLFFIACGGEQKDHGEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTPTPSDIFVSYSTFPFVSMRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAISSLTPTPSDIFVSYSTFPFVSMRDPKSG 360
Qy 361 SWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFEQWHAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

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Db 361 SWYVETLDDIFEOWAHSEDLQSLLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 9
US-10-059-749-2
; Sequence 2, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-May-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-May-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRHMIEDIORAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSSELFRPHMIEDIORAGSGSRDQARQLII 60
QY 61 DLETRGSQLPLFISCLDTGQDMLASFLRTRNQAOKLSKPTLENLTPVVLRLPEIRKPEV 120
DB 61 DLETRGSQLPLFISCLDTGQDMLASFLRTRNQAOKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETRPVDIGSGFGDVGALSLRGNADLAYILSMPCGHCCLIINNVCRESGLRTR 180
DB 121 LRPETRPVDIGSGFGDVGALSLRGNADLAYILSMPCGHCCLIINNVCRESGLRTR 180
QY 181 TGSNDICEKLRRRFSLSLHFMVEVKGDLTAKQVLLALLELARQDHGALDCCVVVILSHGQC 240
DB 181 TGSNDICEKLRRRFSLSLHFMVEVKGDLTAKQVLLALLELARQDHGALDCCVVVILSHGQC 240
QY 241 ASHLQFPGAVYGTGDCPVSVSEKIVNIFNGTSCPSLGKPKLFFIQACGGEQKDHGFEVAS 300
DB 241 ASHLQFPGAVYGTGDCPVSVSEKIVNIFNGTSCPSLGKPKLFFIQACGGEQKDHGFEVAS 300

Db 361 SWYVETLDDIFEOWAHSEDLQSLLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
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QY 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPTSDIFVSYSTFGFVSWRDPKSG 360
 Db 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPTSDIFVSYSTFGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDQSLLLRANAVSVKGYKQMPGCFNFKKLFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDQSLLLRANAVSVKGYKQMPGCFNFKKLFKTS 416

RESULT 10
 US-08-936C-4
 ; Sequence 4, Application US/08852936C
 ; Patent No. 6010878
 ; GENERAL INFORMATION:
 ; APPLICANT: DIXIT, VISHVA M.
 ; APPLICANT: HE, WEI-WU
 ; APPLICANT: KIKLY, KRISTINE K.
 ; APPLICANT: RUBEN, STEVEN M.
 ; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
 ; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852.936C
 ; FILING DATE: 08-MAY-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/018,961
 ; FILING DATE: 05-JUN-1996
 ; APPLICATION NUMBER: 60/020,344
 ; FILING DATE: 23-MAY-1996
 ; APPLICATION NUMBER: 60/017,949
 ; FILING DATE: 20-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: P50483-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 203 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-936C-4

Query Match 49.7%; Score 1083; DI 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2.4e-110;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 212 MYLALLELARQDHGALDCCVVVILSHGCOASHLQPGAVYGTGDCPVSVKEIVNIFNGTS 271
 Db 1 MYLALLELARQDHGALDCCVVVILSHGCOASHLQPGAVYGTGDCPVSVKEIVNIFNGTS 60
 QY 272 CPSLOGKPKLFFIQACGGEQKDHGEVASTSPEDSPGNSPEPDATPFQEGRLTFDQDA 331
 Db 61 CPSLOGKPKLFFIQACGGEQKDHGEVASTSPEDSPGNSPEPDATPFQEGRLTFDQDA 120

QY 332 ISSLPTSDIFVSYSTFGFVSWRDPKSGWYVETLDDIFEQWAHSEDQSLLLRANAV 391
 Db 121 ISSLPTSDIFVSYSTFGFVSWRDPKSGWYVETLDDIFEQWAHSEDQSLLLRANAV 180
 QY 392 SVKGYKQMPGCFNFKKLF 413
 Db 181 SVKGYKQMPGCFNFKKLF 202

RESULT 11
 US-09-300-328-4
 ; Sequence 4, Application US/09300328
 ; Patent No. 6294169
 ; GENERAL INFORMATION:
 ; APPLICANT: DIXIT, VISHVA M.
 ; APPLICANT: HE, WEI-WU
 ; APPLICANT: KIKLY, KRISTINE K.
 ; APPLICANT: RUBEN, STEVEN M.
 ; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
 ; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/300.328
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852.936
 ; FILING DATE: 08-MAY-1997
 ; APPLICATION NUMBER: 60/018,961
 ; FILING DATE: 05-JUN-1996
 ; APPLICATION NUMBER: 60/020,344
 ; FILING DATE: 23-MAY-1996
 ; APPLICATION NUMBER: 60/017,949
 ; FILING DATE: 20-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: P50483-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0700
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 203 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-300-328-4

Query Match 49.7%; Score 1083; DB 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2.4e-110;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 212 MYLALLELARQDHGALDCCVVVILSHGCOASHLQPGAVYGTGDCPVSVKEIVNIFNGTS 271
 Db 1 MYLALLELARQDHGALDCCVVVILSHGCOASHLQPGAVYGTGDCPVSVKEIVNIFNGTS 60
 QY 272 CPSLOGKPKLFFIQACGGEQKDHGEVASTSPEDSPGNSPEPDATPFQEGRLTFDQDA 331

Db 61 CBSLGGKPKLFFIQACGGQKHGEVASTSPEDSPGNSPEPDATPFQEGRLTFDQLDA 120
Qy 332 ISSLTPSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAV 391
Db 121 ISSLTPSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAV 180
Qy 392 SVKGIYKQMPGCCFNFLRKKLFF 413
Db 181 SVKGIYKQMPGCCFNFLRKKLFF 202

RESULT 12
US-08-591-605-2
; Sequence 2. Application US/08591605
; Patent No. 6060238
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING
; TITLE OF INVENTION: APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,605
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KONSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-21036.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-605-2

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

Qy 150 DLAYILMEPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFMVVKGDILTA 209
Db 34 DSNKYMDYPEMGLCIIINNNKFNHKSFTGTSRSGTDVDAANLRETFRNLYKYEVRNKDILTR 93
Qy 210 KKMVLALLELARQDHGALDCCVVVILSHGCCASHLQPCAVYGTGCPVSVVEKIVNIENG 269
Db 94 EEIVELMRDVSKEDHKSRSFVCLLSHGE-----GIIFGTNG-PVDLKKITNFFRG 145
Qy 270 TSCPSLGGKPKLFFIQACGGQKHGEVASTSPEDSPGNSPEPDATPFQEGRLTFDQL 329
Db 146 DCRSLTGKPKLFIQACRGTELDCCGIETDSGVDDM----- 182
Qy 330 DAISLTPSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN 389
Db 183 -ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSMFIQSLCAMLKQYADKLEPFMHILTRVNR 241
Qy 390 AVSVK-----GIYKQMPGCCFNFLRKKLFF 413
Db 242 KVATEFESFSDATFHAKKQIPCIVSMILTKELYF 275

Db 242 KVATEFESFSDATFHAKKQIPCIVSMILTKELYF 275

RESULT 13
US-08-964-308-6
; Sequence 6. Application US/08964308
; Patent No. 6066715
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: ZAMBONI, ROBERT
; TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
; TITLE OF INVENTION: BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J.
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-308-6

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

Qy 150 DLAYILMEPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFMVVKGDILTA 209
Db 34 DSNKYMDYPEMGLCIIINNNKFNHKSFTGTSRSGTDVDAANLRETFRNLYKYEVRNKDILTR 93
Qy 210 KKMVLALLELARQDHGALDCCVVVILSHGCCASHLQPCAVYGTGCPVSVVEKIVNIENG 269
Db 94 EEIVELMRDVSKEDHKSRSFVCLLSHGE-----GIIFGTNG-PVDLKKITNFFRG 145
Qy 270 TSCPSLGGKPKLFFIQACGGQKHGEVASTSPEDSPGNSPEPDATPFQEGRLTFDQL 329
Db 146 DCRSLTGKPKLFIQACRGTELDCCGIETDSGVDDM----- 182
Qy 330 DAISLTPSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN 389
Db 183 -ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSMFIQSLCAMLKQYADKLEPFMHILTRVNR 241
Qy 390 AVSVK-----GIYKQMPGCCFNFLRKKLFF 413
Db 242 KVATEFESFSDATFHAKKQIPCIVSMILTKELYF 275

RESULT 14

US-08-462-969B-4
; Sequence 4, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease: 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentir Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.969B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/334,251
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Andre
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PFI40P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-969B-4

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHGLIINNPNFCRESGLRTRTGSNIDCEKLRFRSSLSHFVVEVKGDLTA 209
Db 34 DNSYKMDYPENGCLIIINNKNFKHSTGMTSRSGTDVDAANLRFRNLKYEVRNKDLTR 93
QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPGAVYGTGDCPVSVEKIVNIFNG 269
Db 94 EEIVELMRDVSKEHRSKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKITIFFRG 145
QY 270 TSCPSLGKPKLFFIOACGGEGKDHGEVASTSPEDSPGNSPEPDATPQEGRLTFDQL 329
Db 146 DRCSLTGPKLFIIOACRGTELDGCIETDSGVDDM----- 182
QY 330 DAISSLPTPSDIFVYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN 389
Db 183 -ACHKIPVEADFLYAYSTAPGYYSWRNSKGSWFIQSLCAMLKQYADKLEFPHILTRVR 241
QY 390 AVSVK-----GIYKQMPGCFNLRKLLFF 413
Db 242 KVATEFEFSFDATFHAKKQIPICIVSMILTKEYL 275

RESULT 15

US-08-964-313-6
; Sequence 6, Application US/08964313
; Patent No. 6114132

; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: GRESSER, MICHAEL
; APPLICANT: KENNEDY, BRIAN
; APPLICANT: NICHOLSON, DONALD
; APPLICANT: RAMACHANDRAN, CHIDAMBARAN
; APPLICANT: SKOREY, KATHRYN
; APPLICANT: FORD-HUTCHINSON, ANTHONY
; TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,313
; FILING DATE: 04-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,408
; FILING DATE: 04-NOV-1996
; APPLICATION NUMBER: PCT/CA97/00825
; FILING DATE: 03-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DURETTE, PHILIPPE L.
; REGISTRATION NUMBER: 35,125
; REFERENCE/DOCKET NUMBER: 19824Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-4008
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-313-6
Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHGLIINNPNFCRESGLRTRTGSNIDCEKLRFRSSLSHFVVEVKGDLTA 209
Db 34 DNSYKMDYPENGCLIIINNKNFKHSTGMTSRSGTDVDAANLRFRNLKYEVRNKDLTR 93
QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPGAVYGTGDCPVSVEKIVNIFNG 269
Db 94 EEIVELMRDVSKEHRSKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKITIFFRG 145
QY 270 TSCPSLGKPKLFFIOACGGEGKDHGEVASTSPEDSPGNSPEPDATPQEGRLTFDQL 329
Db 146 DRCSLTGPKLFIIOACRGTELDGCIETDSGVDDM----- 182
QY 330 DAISSLPTPSDIFVYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN 389
Db 183 -ACHKIPVEADFLYAYSTAPGYYSWRNSKGSWFIQSLCAMLKQYADKLEFPHILTRVR 241
QY 390 AVSVK-----GIYKQMPGCFNLRKLLFF 413
Db 242 KVATEFEFSFDATFHAKKQIPICIVSMILTKEYL 275

Search completed: October 20, 2003, 12:14:51
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2003, 12:00:41 ; Search time 85 Seconds
(Without alignments)
776,827 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRCRLVLEL.....YKMPGCFNLRKLLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2180	100.0	416	19 AAW39209	Human ICE LAP-6 po
2	2180	100.0	416	22 AAE00620	Human caspase-9, a
3	2157	98.9	416	20 AAY21723	Amino acid sequenc
4	2157	98.9	416	23 ABJ01224	Human caspase-9 SE
5	2153	98.8	416	22 AAE08938	Mammalian ced-3 ho
6	2153	98.8	416	22 AAG67375	Amino acid sequenc
7	2153	98.8	416	22 AAB84374	Amino acid sequenc
8	2153	98.8	416	22 AAU08315	Human aspartate-ep
9	2153	98.8	416	24 ABB82738	Human caspase-9 po

10	1288	59.1	266	22	AAE00620	Human caspase-9.
11	1083	49.7	203	19	AAW39209	Human ICE LAP-6 am
12	468	21.5	93	23	ABJ04760	Caspase-9 protein
13	420	19.3	277	22	AAW39209	Pig caspase #2. S
14	418	19.2	249	21	AAW39209	Human caspase-1 pr
15	418	19.2	277	17	AAW00372	Apoptin CPP12beta
16	418	19.2	277	17	AAW16600	Apoptin CPP12a pro
17	418	19.2	277	17	AAW00677	Pro-Yama. Homo sa
18	418	19.2	277	17	AAW39209	Human interleukin-
19	418	19.2	277	19	AAW41688	Amino acid sequenc
20	418	19.2	277	20	AAU21717	Amino acid sequenc
21	418	19.2	277	22	AAU05394	Human caspase 3.
22	418	19.2	277	22	AAU05395	Mouse caspase 3.
23	418	19.2	277	22	AAE00600	Human caspase-3.
24	418	19.2	277	23	ABG10904	Human membrane der
25	418	19.2	277	23	ABJ01218	Human caspase-3 SE
26	416.5	19.1	245	22	AAW39209	Human caspase-3.
27	414.5	19.0	261	22	AAE00610	Chimeric cassette
28	414	19.0	241	22	AAW39209	Caspase-3. Uniden
29	411	18.9	452	23	ABJ01110	Mouse caspase-2 pr
30	409	18.8	277	19	AAW47089	Rat interleukin-1
31	409	18.8	435	16	AAW66771	Human interleukin-
32	409	18.8	435	17	AAW98462	Human Ice-ced-3 ho
33	409	18.8	435	18	AAW26274	Cell death protein
34	409	18.8	435	20	AAV21716	Amino acid sequenc
35	409	18.8	435	21	AAW14257	Human Ich-1L prote
36	409	18.8	435	22	AAE00599	Human caspase-2, a
37	409	18.8	435	23	ABJ_1217	Amino acid sequenc
38	409	18.8	435	23	ABJ_1217	Human caspase-2 SE
39	409	18.8	441	16	AAW_5768	Human interleukin-
40	409	18.8	441	21	AAW_4253	Human Ich-1 protei
41	408	18.7	277	19	AAW48945	Mutant human apopa
42	408	18.7	277	19	AAW48937	Mutant human apopa
43	405	18.6	435	17	AAW90703	Interleukin-1-beta
44	401.5	18.4	505	15	AAW47463	Ced-3. Caenorhabd
45	395.5	18.1	503	21	AAW14247	Ced-3 protein. Ca

ALIGNMENTS

RESULT 1
AAW39209
ID AAW39209 standard; peptide: 416 AA.
AC AAW39209;

DT 18-MAY-1998 (first entry)

DE Human ICE LAP-6 polypeptide.

XX ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;

KW viral infection; tumour; inflammation; osteoporosis; AIDS; human;

XX Alzheimer's disease.

OS Homo sapiens.

XX EP808904-A2.

XX 26-NOV-1997.

XX 19-MAY-1997; 97EP-0303397.

XX 05-JUN-1996; 96US-0018961.

XX 20-MAY-1996; 96US-0017949.

XX 23-MAY-1996; 96US-0020344.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (SHIK) SMITHKLINE BEECHAM CORP.

XX (UNMI) UNIV MICHIGAN.

XX Dixit VM, He W, Kikly KK, Ruben SM;


```
07-MAR-2003 (first entry)
Human caspase-9 polypeptide.
Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac;
human.
Homo sapiens.
OS
XX
WO200290931-A2.
PN
XX
PD
14-NOV-2002.
PP
07-MAY-2002; 2002WO-US14487.
XX
07-MAY-2001; 2001US-289223P.
PPR
12-FEB-2002; 2002US-356934P.
PP
(BURN-) BURNHAM INST.
XX
Reed JC;
WPI; 2003-111999/10.
XX
Determining a prognosis for survival for a cancer patient, useful for
determining if the patient is at risk for relapse, comprises measuring
a level of TUCAN in a sample from the patient, and comparing it to a
reference level.
XX
Examples; Page 125-126; 153pp; English.
XX
The invention relates to determining a prognosis for survival for a
cancer patient. The method involves (a) measuring a level of a tumour up-
regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
cell-containing sample from the cancer patient, and (b) comparing the
level of TUCAN in the sample to a reference level of TUCAN, where a low
level of TUCAN in the sample correlates with increased survival of the
patient. Alternatively, the method involves measuring levels of TUCAN and
one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
Smac in a neoplastic cell-containing sample from the cancer patient. The
method is useful for determining if the patient is at risk for relapse,
or for determining a proper course of treatment for a patient with
cancer. The method is also useful for monitoring the effectiveness of a
course of treatment for a patient with cancer, e.g. colon cancer,
gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
present sequence represents a human caspase-9 polypeptide.
XX
Query Match 98.8%; Score 2153; DB 24; Length 416;
Best Local Similarity 98.8%; Pred No. 2, 9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Sequence 416 AA:
1 MDEADRLRLRCRLRVLEQVLDVQDVLVLLGRELFRPHMIEDIQAGSGRRDQARQLII 60
1 MDEADRLRLRCRLRVLEQVLDVQDVLVLLGRELFRPHMIEDIQAGSGRRDQARQLII 60
61 DLETRGSQALPLFISCLDGTGDMVLASFLRTRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
61 DLETRGSQALPLFISCLDGTGDMVLASFLRTRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
121 LRPETPRPVDTGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLIIINNVNFCRESGLRTR 180
121 LRPETPRPVDTGSGGFGDVGALSLRGNADLAYILSMPEPCGHCLIIINNVNFCRESGLRTR 180
181 TGSNDICEKLRRRFSLSHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQC 240
181 TGSNDICEKLRRRFSLSHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQC 240
241 ASHLQFPAGVYGTDCPCPSVVEKIYVNFNGTSCPSLGGPKLFFFIQACGGEQKDHGFEVAS 300
241 ASHLQFPAGVYGTDCPCPSVVEKIYVNFNGTSCPSLGGPKLFFFIQACGGEQKDHGFEVAS 300
QY 301 TSPEDSGSNPEPDATPFQEGRLTTPQOLAISLPTSPDIFVSYSTPFGVSWRDPKSG 360
DB 301 TSPEDSGSNPEPDATPFQEGRLTTPQOLAISLPTSPDIFVSYSTPFGVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWHSDELQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
DB 361 SWYVETLDDIFEQWHSDELQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
RESULT 10
AAE00620
ID AAE00620 standard; Protein: 266 AA.
XX
AC AAE00620;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human caspase-9.
XX
KW Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Cleavage-site 165..166 /label= Proteolytic_cleavage_site
FT Cleavage-site 180..181 /label= Proteolytic_cleavage_site
FT FT
PN WO200129232-A2.
XX
PD 26-APR-2001.
XX
PF 19-OCT-2000; 2000WO-US28941.
PR 20-OCT-1999; 99US-0160559.
PR 14-AUG-2000; 2000US-0225564.
XX
PA (SCIO-) SCIOS INC.
XX
PI Cordell B, Li Y;
XX
DR WPI; 2001-290920/30.
DR N-PSDB; AAD03916.
XX
Novel fusion polypeptide comprising first and second caspase subunit
separated by cleavage site not associated in nature with caspase
subunit, useful for cloning gene encoding enzymes involved in
proteolytic cleavage.
Claim 4; Page 105-107; 116pp; English.
The present amino acid sequence is human Caspase-9 also known as
interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases are
a family of cysteine proteases, that participate in the initiation and
execution of apoptosis. Caspases exist as pro-enzymes, activated by
cleavage into a large and small subunit, occurring after specific
aspartic acid residues within the pro-enzyme sequence.
The present invention relates to a method for functional cloning of genes
encoding proteins or enzymes involved in proteolytic cleavage. The
invention is based on the use of caspase expression cassettes comprising
the coding sequence of a proteolytic cleavage site flanked by sequences
encoding two caspase subunits. A fusion polypeptide comprising a first
and a second caspase subunit, separated by a cleavage site not associated
in nature, is useful for cloning gene encoding enzymes involved in
proteolytic cleavage. An express on cassette containing fusion
polypeptide is used to identify a mutant cell line deficient in an
enzyme of interest and is also useful for diagnosis and suppression of
proliferation or metastases of a tumour cell characterised by
overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
```

CC selectively expressed in the tumour cells). DNA encoding fusion
 CC polypeptide is used in gene therapy.
 CC Note: This sequence SEQ.ID.NO.18 is stated as being the same as that
 CC shown in Figure 18 (See AAE00606) in the specification. However these
 CC sequences differ at several positions.

XX Sequence 266 AA;

Query Match 59.1%; Score 1288; DB 22; Length 266;
 Best Local Similarity 63.5%; Pred. No. 1.5e-126;
 Matches 264; Conservative 0; Mismatches 2; Indels 150; Gaps 1;

QY 1 MDEADRLRLRCRLRVEELVDQLMDVLLSRFLFRPHMIEDIQAGSGSRDQARQLII 60
 DB 1 MDEADRLRLRCRLRVEELVDQLMDVLLSRFLFRPHMIEDIQAGSGSRDQARQLII 60
 QY 61 DLETRGSQLPLFISCLEDTGDMILASFLRTNRQAGLSKPTLENLTPVVLRLPEIRKKEV 120
 DB 61 DLETRGSQLPLFISCLEDTGDMILASFLRTNRQAGLSKPTLENLTPVVLRLPEIRKKEV 120
 QY 121 LRPETPRVDIGSGGDDVCALESRLGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
 DB 121 LRPETPRVDIGSGGDDVCALESRLGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
 QY 181 TGSNIDCEKLRRRFSLLHFMEVKGDLTAKOMVLALELARDHGDALDCCVVILSHGCG 240
 DB 140 -----EQKDHGFEVAS 150
 QY 241 ASHLQFPGAVYGTGDCPVSVKEIWNIFNGTSCPS .3GKPKLFFIOACGGEQKDHGFEVAS 300
 DB 140 -----EQKDHGFEVAS 150
 QY 301 TSPDESFGSNPEPDATPQEGLRTFDQDAISSLPTPSDIFVSYSTFPFGVSWI .PKSG 360
 DB 151 TSPDESFGSNPEPDATPQEGLRTFDQDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 210
 QY 361 SWVETLDDIIFEQWASEDLQSLLLRVANAVSVKGIYKOMPFCNFKLKKLFKTS 416
 DB 211 SWVETLDDIIFEQWASEDLQSLLLRVANAVSVKGIYKOMPFCNFKLKKLFKTS 266

RESULT 11
 AAW39208
 ID AAW39208 standard; peptide; 203 AA.
 AC AAW39208;
 DT 18-MAY-1998 (first entry)
 DE Human ICE LAP-6 amino acid sequence variant.
 KW ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
 KW viral infection; tumour; inflammation; osteoporosis; AIDS; human;
 KW Alzheimer's disease; variant.

XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 203 /note= "encoded by TAA"
 FT
 XX EP080904-A2.
 XX
 XX 26-NOV-1997.
 XX
 XX 19-MAY-1997; 97EP-0303397.
 XX
 XX 05-JUN-1996; 96US-0018961.
 XX 20-MAY-1996; 96US-0017949.
 XX 23-MAY-1996; 96US-0020344.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (UNMI) UNIV MICHIGAN.
 XX Dixit VM, He W, Kikly KK, Ruben SM;
 XX WPI; 1998-001790/01.
 DR N-PSDB; AAV09402.
 XX
 PT DNA encoding interleukin-1 beta converting enzyme apoptosis
 PT protease-6 - useful to develop products to treat, e.g. viral
 PT infection, tumour, Alzheimer's disease, inflammation, osteoporosis
 PT and AIDS
 XX
 PS Disclosure; Fig 5; 44pp; English.
 XX
 CC This is an amino acid sequence variant of human interleukin-1 beta
 CC converting enzyme apoptosis protease-6 (ICE LAP-6) polypeptide. The ICE
 CC LAP-6 polypeptide and agonists to the polypeptide can be used to induce
 CC apoptosis, e.g. as an antiviral or antitumour agent, control embryonic
 CC development and tissue homeostasis and the roles of such factors in
 CC dysfunction and disease. Antagonists which inhibit the activity of the
 CC ICE LAP-6 polypeptide can be used to treat, Alzheimer's or Parkinson's
 CC disease, rheumatoid arthritis, septic shock, stroke, chronic,
 CC acute or central nervous system inflammation, osteoporosis, ischaemia
 CC reperfusion injury, cell death associated with cardiovascular disease,
 CC polycystic kidney disease, apoptotic of endothelial cells in
 CC cardiovascular disease, degenerative liver disease, multiple sclerosis,
 CC cerebellar degeneration ischaemic injury, myocardial infarction,
 CC acquired immunodeficiency syndrome (AIDS), myelodysplastic syndrome,
 CC aplastic anaemia, male pattern baldness and head injury damage. They can
 CC also be used for detection and diagnosis.

SQ Sequence 203 AA;

Query Match 49.7%; Score 1083; DB 19; Length 203;
 Best Local Similarity 100.0%; Pred. No. 3.7e-105;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 MYLALLELARODHGDALDCCVVVILSHGCGASHLOFPGAVYGTGDCPVSVKEIWNIFNGTS 271
 DB 1 MYLALLELARODHGDALDCCVVVILSHGCGASHLOFPGAVYGTGDCPVSVKEIWNIFNGTS 60
 QY 272 CPSLGGKPKLFFIOACGGEQKDHGFEVASTSPDESFGSNPEPDATPQEGLRTFDQDA 331
 DB 61 CPSLGGKPKLFFIOACGGEQKDHGFEVASTSPDESFGSNPEPDATPQEGLRTFDQDA 120
 QY 332 ISSLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIIFEQWASEDLQSLLLRVANAV 391
 DB 121 ISSLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIIFEQWASEDLQSLLLRVANAV 180
 QY 392 SVKGIYKOMPFCNFKLKKLFF 413
 DB 181 SVKGIYKOMPFCNFKLKKLFF 202

RESULT 12
 ABJ04760
 ID ABJ04760 standard; Protein; 93 AA.
 XX
 AC ABJ04760;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 XX Caspase-9 protein sequence SEQ ID No 27.

KW Intracellular signaling polypeptide; Nod2; Crohn's disease; mutation;
 KW cytosine residue insertion; nuclear factor; NF-B activation; NF-kappa B;
 KW RICK signaling; gene therapy; transgenic plant; plant.
 OS Homo sapiens.
 XX WO200244426-A2.
 PN 06-JUN-2002.
 PD

210 KMYLALLELAEARODHGALDCCVWVILSHCQASHLOFPGAVYGTDCPCVSVYKIVNIENG 269
94 EEIVELMRDVSKEHSHKSSFCVLLSHGEE-----GIIFGTNG-PVDLKKITNFRG 145
270 TSCPSLGGKPKLFFIQACGGEOKDHGFVASTSPESPGSNPEPDATPFQEGRLTFDOL 329
146 DRCRSLTGPKLFIQACRGTELDGIEGDSGVDDM----- 182
330 DAISLPTPSDIFVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVAN 389
183 -ACHKIPVEADFLYAYSTAPGYYSWRNSKDSWFTQSLCAMLKQYADKLEFMHILTRVNR 241
390 AVSVK-----GIYKQMPGCFNFLRKLFF 413
242 KVATEFESFDFATTHAKKQIPCIIVSMLTKELYF 275

Search completed: October 20, 2003, 12:11:09
Job time : 87 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2003, 12:01:16 ; Search time 24 Seconds
(without alignments)
815.130 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCGNFRLRKLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2166	99.4	416	1 ICE9_HUMAN	P55211 homo sapien
2	465	21.3	424	1 ICE2_CHICK	Q98943 gallus gall
3	428	19.6	277	1 ICE3_CRILLO	Q60431 cricetus
4	418	19.2	277	1 ICE3_HUMAN	P42574 homo sapien
5	418	19.2	277	1 ICE3_MOUSE	P70677 mus musculus
6	411	18.9	435	1 ICE2_MOUSE	P29594 mus musculus
7	409	18.8	277	1 ICE3_RAT	P55213 rattus norv
8	409	18.8	435	1 ICE2_HUMAN	P42575 homo sapien
9	407	18.7	496	1 ICE3_CAEVU	P45436 caenorhabdi
10	389.5	17.9	480	1 ICE8_MOUSE	O89110 mus musculus
11	387.5	17.8	503	1 ICE3_CAEEL	P42573 caenorhabdi
12	383	17.6	479	1 ICE8_HUMAN	Q14790 h caspase-8
13	364.5	16.7	303	1 ICE7_MESAU	P55214 mesocricetu
14	361.5	16.6	303	1 ICE7_HUMAN	P55210 homo sapien
15	350.5	16.1	303	1 ICE7_MOUSE	P97864 mus musculus
16	349	16.0	282	1 ICE3_XENLA	P55866 xenopus lae
17	324	14.9	339	1 ICE_DROME	O01382 drosophila
18	322	14.8	276	1 ICE6_MOUSE	O08738 mus musculus
19	320	14.7	323	1 ICE1_DROME	O02002 drosophila
20	312.5	14.3	312	1 ICE2_RAT	P55215 rattus norv
21	311.5	14.3	293	1 ICE6_HUMAN	P55212 homo sapien
22	305	14.0	521	1 ICEA_HUMAN	Q92851 homo sapien
23	300.5	13.8	405	1 IIBC_HORSE	Q9tvl3 equus caball
24	297.5	13.6	299	1 ICE1_SPOFR	P89116 spodoptera
25	279	12.8	382	1 ICEB_XENLA	P55867 xenopus lae
26	278	12.8	404	1 IIBC_PIG	Q9n2il sus scrofa
27	274	12.6	410	1 IIBC_FELCA	Q9mzv6 felis silve
28	270.5	12.4	402	1 IIBC_RAT	P43527 rattus norv
29	268.5	12.3	402	1 IIBC_MOUSE	P29452 mus musculus
30	262	12.0	404	1 IIBC_CANFA	Q9mzv7 canis fami
31	259	11.9	404	1 IIBC_HUMAN	P29466 homo sapien
32	256	11.7	386	1 ICEA_XENLA	P55865 xenopus lae
33	253	11.6	257	1 ICEE_MOUSE	O89094 mus musculus

RESULT 1

ID	ICE9_HUMAN	STANDARD;	PRT;	416 AA.
AC	P55211; Q95348; Q92852; Q9BQ62; Q9UEQ3; Q9UIJ8;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease activating factor 3) (A'AF-3).			
GN	CASP9 OR MCH6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.			
RX	MEDLINE=96279246; PubMed=8663294;			
RA	Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,			
RA	He W.-W., Dixit V.M.;			
RT	"ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated by the cytotoxic T cell protease granzyme B.";			
RL	J. Biol. Chem. 271:16720-16724(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97059171; PubMed=8900201;			
RA	Srinivasulu S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,			
RA	Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,			
RA	Alnemri E.S.;			
RT	"The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic mediator CPP32.";			
RL	J. Biol. Chem. 271:27099-27106(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99315341; PubMed=10384055;			
RA	Hadano S., Naair J., Nichol K., Rasper D.M., Vaillancourt J.P.,			
RA	Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;			
RT	"Genomic organization of the human caspase-9 gene on chromosome 1p36.1-p36.3.";			
RL	Mamm. Genome 10:757-760(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=99168502; PubMed=10070954;			
RA	Srinivasulu S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,			
RA	Fernandes-Alnemri T., Alnemri E.S.;			
RT	"Identification of an endogenous dominant-negative short isoform of caspase-9 that can regulate apoptosis.";			
RL	Cancer Res. 59:999-1002(1999).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Stomach cancer;			
RA	Izawa M., Mori T., Ito H., Sairenji T.;			
RT	"Molecular cloning and sequencing of a cDNA predicting an alternative form of pro-caspase-9 from human gastric cancer cell lines.";			

ALIGNMENTS

34	239.5	11.0	242	1	ICEE_HUMAN	P31944 homo sapien
35	232	10.6	377	1	ICED_BOVIN	O75601 bos taurus
36	212	8.7	373	1	ICEB_MOUSE	P70343 mus musculus
37	210	9.6	418	1	ICE5_HUMAN	P51878 homo sapien
38	209	9.6	377	1	ICE4_HUMAN	P49662 homo sapien
39	207	9.5	419	1	ICEC_MOUSE	O08736 mus musculus
40	165	7.6	484	1	CFLA_MOUSE	O35732 m casp8 and
41	147	6.7	480	1	CFLA_HUMAN	O15519 h casp8 and
42	113.5	5.2	1612	1	RPO_ORSVS	O84133 odontogloss
43	106.5	4.9	589	1	RGP1_MOUSE	P46061 mus musculus
44	97.5	4.5	382	1	ANAC_HUMAN	Q9uhk6 homo sapien
45	94	4.3	950	1	ORP1_HUMAN	Q9bxb6 homo sapien


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Query Match      99.4%; Score 2166; DB 1; Length 416;
Best Local Similarity 99.3%; Pred. No. 5.9e-177;
Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEADRLRLRLRLVEELQVDQDMLASFLTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 60
   |||||
Db 1 MDEADRLRLRLRLVEELQVDQDMLASFLTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 60

QY 61 DLTRGSOALPLFISCLDQDMLASFLTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
   |||||
Db 61 DLTRGSOALPLFISCLDQDMLASFLTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120

QY 121 LRPETPRVDIGSGFGDVGALSLRGNADLAYILSMPCGHCLIIINNFCRESGLRTR 180
   |||||
Db 121 LRPETPRVDIGSGFGDVGALSLRGNADLAYILSMPCGHCLIIINNFCRESGLRTR 180

QY 181 TGSNIDCEKLRRLRRLSSLFHFMVEVKGDLTAKQWLLALLELAFQDHDGALDCCVVILSHGCC 240
   |||||
Db 181 TGSNIDCEKLRRLRRLSSLFHFMVEVKGDLTAKQWLLALLELAFQDHDGALDCCVVILSHGCC 240

QY 241 ASHLQFPGAVYGTDCPVSVEKIWNIFNGTSCPSLGKPKLFFITQACGGQKHGFVEAS 300
   |||||
Db 241 ASHLQFPGAVYGTDCPVSVEKIWNIFNGTSCPSLGKPKLFFITQACGGQKHGFVEAS 300

QY 301 TSPEDSPGSPNEPDATPFQGLRTFDQDLSLTPSDIFVSYSYTFPGFVSRDPKSG 360
   |||||
Db 301 TSPEDSPGSPNEPDATPFQGLRTFDQDLSLTPSDIFVSYSYTFPGFVSRDPKSG 360

QY 361 SWYVETLDDIFEQWHAHSEDLSLLLRVANAVS; ;YKQMPGCFNFKLFFKTS 416
   |||||
Db 361 SWYVETLDDIFEQWHAHSEDLSLLLRVANAVS; ;YKQMPGCFNFKLFFKTS 416

RESULT 2
ICE2_CHICK
ID ICE2_CHICK STANDARD; PRT; 424 AA.
AC Q98943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
DE Gallus.
GN CASP2 OR ICH1.
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
RC STRAIN=White leghorn; TISSUE=Ovarian granulosa;
RX MEDLINE=97368127; PubMed=9224894;
RA Johnson A.L., Bridgman J.T., Bergeron L., Yuan J.;
RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary.";
RL Gene 192:227-233(1997).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=ICH-1L;
CC IsoId=Q98943-1; Sequence=Displayed;
CC Note=Only form found in the ovary;
CC Name=ICH-1S;
CC IsoId=Q98943-2; Sequence=VSP_000803, VSP_000804;
CC -!- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U64963; AAC29881.1; ALT_INIT.
CC HSP; P42574; ICP3.
CC MEROPS; C14.006; -.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR002398; ICE.
CC InterPro: IPR021138; ICE_P10.
CC InterPro: IPR001309; ICE_P20.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00656; Peptidase C14; 1.
CC PRINTS; PR00376; IL1BCENZYME.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS0209; CARD; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS0207; CASPASE_P10; 1.
CC PROSITE; PS0208; CASPASE_P20; 1.
CC Hydroxylase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
KW PROPEP 1 140
FT CHAIN 141 308
FT CHAIN 309 424
FT CHAIN 315 424
FT DOMAIN 7 96
FT ACT_SITE 248 248
FT ACT_SITE 291 291
FT VARSPPLIC 1 7
FT VARSPPLIC 294 424
FT VARSPPLIC 424 424
FT DETDRGVDRDQKERSDSDPGCEESDANKEENLKLRLPTRSD
FT MICGVACLKGTAAAMNTRKGSWYIEALTTFVAFDSRDTHVA
FT DMLVKVNRQIKOREGYAPCTEPRCKEMSEYCVSTLCRLDLYL
FT FPGYVPGK -> GVSGIHIHLPLCCCHICCSMPTGTGEWI
FT REMAKNGQIPQARRVMOTIRKKISSVCVCHAPI (in
FT isoform ICH-1S).
FT /FTID=VSP_000804.
SQ SEQUENCE 424 AA; 47959 MW; 7928105088B3F60 CRC64;

Query Match      21.3%; Score 465; DB 1; Length 424;
Best Local Similarity 30.7%; Pred. No. 5.3e-32;
Matches 128; Conservative 73; Mismatches 172; Indels 44; Gaps 12;

QY 1 MDEADRLRLRLRLVEELQVDQDMLASFLTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 59
   |||||
Db 7 MQRVHQEALKKNRVMLARELVKLMEHMKDIIETIEMVEMIOAKSGSFQNVFNL- 65

QY 60 IDLETRGSOALPLFISCLDQDMLASFLTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 114
   |||||
Db 66 --LPKRGPNFAFSAFCEALQETKQKHLAEMILKTESSLRHGIATLEQRYGSLN-PLPL- 119

QY 115 IRKPEVLRPETPRVDIGSGFGDVGAL-----ESLRGNADLAYILSMPCGHCLII 166
   |||||
Db 120 ---SSCSKSRPLRIVEHSLSGDGPPIPVKHCTPEYRDHOLHAYKLISEPGLALIL 176

QY 167 NNVNFRCRSGURTRTGSNIDCEKLRRLRRLSSLFHFMVEVKGDLTAKQWLLALLELAFQDHDG 225
   |||||
Db 177 SNHFSEKDLRYRSGDVGDCASLELLFKHLGYQVTVFHDQSABEMESALERFRLPDHQ 236

QY 226 ALDCCVVILSHGCCASHLQFPGAVYGTDCPVSVEKIWNIFNGTSCPSLGKPKLFFITQACGG 285
   |||||
Db 237 DVDSCIVALLSHGVE-----GGVYGTGKLLQLQEAFLRFDNANNCNQLQKPKHFFIQ 289

QY 286 ACCGQKHGFVEASTSPEDSPGSPNEPDATPFQGLRTFDQDLSLTPSDIFVSYSYTFPGFVSRDPKSG 345
   |||||
Db 290 ACRGDETDRGVDRDQKERSDSDPGCE-ESDANK-EENLKL-----RLPTRSDMICGY 339

QY 346 STFPQFVSRDPKSGSWYVETLDDIFEQWHAHSEDLSLLLRVANAVS; ;YKQMPGCFNFKLFFKTS 402
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Db 340 ACLKGTAAARNTRKSGMYREALITVPAEDSRDT VADMLVKVNQIKOREGY--APG 394
RESULT 3
ICE3_CRIL0
ID ICE3_CRIL0 STANDARD: PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
DE (SCA-1).
OS Crisp3 OR Cpp32.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=9618185; PubMed=8605870;
RA Wang X., Zelenski N.G., Yang J., Sakai J., town M.S.,
RA Goldstein J.L.;
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis."
RL EMBL J. 15:1012-1020(1996).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEPTASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROPEPTASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch].
CC
CC EMBL: U27463; AAB01511.1;
CC HSSP: P42574; 1PAU.
CC MEROPS: C14.003;
CC InterPro: IPR002398; ICE.
CC InterPro: IPR00138; ICE_p10.
CC InterPro: IPR001309; ICE_p20.
CC Pfam: PF00656; Peptidase_C14; 1.
CC PRINTS: PR00376; ILIBENZYM.
CC SMART: SM00115; CASP; 1.
CC PROSITE: PS01122; CASPASE_CYS; 1.
CC PROSITE: PS01121; CASPASE_HIS; 1.
CC PROSITE: PS50207; CASPASE_P10; 1.
CC PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apopto s.
FT PROPEP 1 9 BY SIMILARITY
FT PROPEP 10 28 BY SIMILARITY
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.

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PT ACT SITE 163 163 BY SIMILARITY.
SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 19.6%; Score 428; DB 1; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.2e-29;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAIVLSMEPCGCHLIINNVNFCRESGLRTRTCSNIDCEKLRERFSSLHFMVEVKGLTA 209
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 34 DSSVMDYPMGVGCIINNNKFNHKTGTPRSGTDVDAKLRFTFPAIKYEVNKNDLTR 93
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 210 KMYLALLELARQDHGALDCVVVYILSHGQASHLOFPGAVYGTDCGPVSVEKIVNIFNG 269
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 94 BEIVELMKNAKSKDHKSRSFVVCVILSHGDE-----GVIFCTDG-PIDLKGLTSYFRG 145
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 270 TSCPSLGGKPKLFFIOACGGEQKHDFEAVASTSPEDSPGNSPEPDATPQEGRLTFDQL 329
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 146 DYCNSLIGKPKLFFIQACRGTELDGCIETSDGTEDDMT----- 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 DAISLTPSDIFVSYSTFPFVSWRDPKSGSVWVETLDDIFEQWAHSEDLOSLLLRVAN 389
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 --COKIPVEADFLVAYSTAFGYYSWRNPKGDSNFIQSLCSMLKLYAKHLEFVGHILTRVR 241
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 AVSVK-----GIYKMPGCGFNLKRLFF 413
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 242 KVATEFESFSLDSTFHAKQIQCIVSMLTKELVF 275
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
ICE3_HUMAN
ID ICE3_HUMAN STANDARD; PRT; 277 AA.
AC P42574; Q96AN1; O96KP2;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
DE (SCA-1).
GN CASP3 OR CPP32.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT interleukin-1 beta-converting enzyme."
RT J. Biol. Chem. 269:30761-30764(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase."
RL Cell 81:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Vallette F.M., Oliver L.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA	Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	RT	is modulated by the polyglutamine tract.;
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,	RL	Nat. Genet. 13:442-449(1996).
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,	CC	FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,	CC	RESPONSIBLE FOR APOPTOSIS EXECUTION AT THE ONSET OF APOPTOSIS IT
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,	CC	PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
RA	Raba S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaly S.J.,	CC	216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	CC	ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	CC	HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
RA	Villalon D.J., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	CC	CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
RA	Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	CC	CLEAVAGE OF HUNTINGTIN.
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	CC	ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
RA	Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,	CC	SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	CC	SUBCELLULAR LOCATION: Cytoplasmic.
RA	Butterfield Y.S.N., Kryzhanvski M.I., Skalska U., Smalley D.E.,	CC	TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.,	CC	AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW
RT	"Generation and initial analysis of more than 15,000 full-length	CC	IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN
RT	human and mouse cDNA sequences."	CC	CELLS OF THE IMMUNE SYSTEM.
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	CC	PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
RP	SEQUENCE OF 29-46 AND 175-193. AND FUNCTION.	CC	GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
RX	MEDLINE=95319529; PubMed=7596430;	CC	PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
RA	Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,	CC	ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
RA	Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,	CC	OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
RA	Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,	CC	AND VICE VERSA.
RA	Miller D.K.;	CC	SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
RT	"Identification and inhibition of the ICE/CED-3 protease necessary	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RT	for mammalian apoptosis."	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RL	Nature 376:37-43(1995).	CC	the European Bioinformatics Institute. There are no restrictions on its
RN	[6]	CC	use by non-profit institution as long as its content is in no way
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.	CC	modified and this statement is not removed. Usage by and for commercial
RP	MEDLINE=96266352; PubMed=8673606;	CC	entities requires a license agreement (See http://www.iab-sib.ch/announce/
RA	Recondia J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,	CC	or send an email to license@iab-sib.ch).
RA	Labelle M., Peterson E.P., Raepier D.M., Ruel R., Vaillancourt J.P.,	CC	EMBL; U13737; AAA65015.1; -
RA	Thornberry N.A., Becker J.W.;	CC	EMBL; U13738; AAB60355.1; -
RT	"The three-dimensional structure of apopain/CPP32, a key mediator of	CC	EMBL; U26943; AAA74929.1; -
RT	apoptosis."	CC	EMBL; AJ413269; CAC88866.1; -
RL	Nat. Struct. Biol. 3:619-625(1996).	CC	EMBL; BC016926; AAH16926.1; -
RP	[7]	DR	PIR; A55315; A55315.
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.	DR	PDB; 1PAU; 07-JUL-97.
RX	MEDLINE=97197830; PubMed=9045680;	DR	PDB; 1CP3; 24-DEC-97.
RA	Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,	DR	PDB; 1GFW; 23-JUN-00.
RA	Priestle J.P., Tomaselli K.J., Grutter M.G.;	DR	MEROPS; C14.003; -
RT	"Structure of recombinant human CPP32 in complex with the	DR	Genew; HGNC:1504; CASP.
RT	tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone."	DR	MIM; 606336; -
RL	J. Biol. Chem. 272:6539-6547(1997).	DR	GO; GO:0004208; F:caspase-3 activity; TAS.
RP	[8]	DR	GO; GO:0008624; P:induction of apoptosis by extracellular sig. ; TAS.
RX	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).	DR	GO; GO:0009405; P:pathogenesis; TAS.
RX	MEDLINE=20283632; PubMed=10821855;	DR	InterPro; IPR002398; ICE.
RA	Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,	DR	InterPro; IPR002138; ICE p10.
RA	Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,	DR	InterPro; IPR001309; ICE p20.
RA	Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,	DR	Pfam; PF00656; Peptidase_C14; 1.
RA	Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,	DR	PRINTS; PR00376; ILIBCEZYME.
RA	Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,	DR	SMART; SM00115; CASC; 1.
RA	Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;	DR	PROSITE; PS01122; CASPASE_CYS; 1.
RT	"Potent and selective nonpeptide inhibitors of caspases 3 and 7	DR	PROSITE; PS01121; CASPASE_HIS; 1.
RT	inhibit apoptosis and maintain cell functionality."	DR	PROSITE; PS50207; CASPASE_P10; 1.
RL	J. Biol. Chem. 275:16007-16014(2000).	DR	PROSITE; PS50208; CASPASE_P20; 1.
RP	[9]	KW	Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
RP	PROCESSING.	KW	3D-structure.
RX	MEDLINE=96335388; PubMed=8755496;	FT	PROPEP 1 9
RA	Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,	FT	PROPEP 10 28
RA	Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,	FT	CHAIN 29 175
RA	Litwack G., Alnemri E.S.;	FT	CHAIN 176 277
RT	"In vitro activation of CPP32 and Mch3 by Mc14, a novel human	FT	ACT_SITE 121 121
RT	apoptotic cysteine protease containing two FADD-like domains."	FT	ACT_SITE 163 163
RL	Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).	FT	VARIANT 190 190
RN	[10]	FT	CONFLICT 31 36
RP	CLEAVAGE OF HUNTINGTIN.	FT	STRAND 36 36
RX	MEDLINE=96331285; PubMed=8696339;	FT	STRAND 43 51
RA	Goldberg Y.P., Nicholson D.W., Raepier D.M., Kalchman M.A., Koide H.B.,	FT	HELIX 57 59
RA	Graham R.K., Brown M., Kazemi-Esfarjani P., Thornberry N.A.,		
RA	Vaillancourt J.P., Hayden M.R.;		
RT	"Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,		

FT TURN 60 60
 FT TURN 65 66
 FT HELIX 67 80
 FT TURN 81 82
 FT STRAND 84 89
 FT HELIX 93 104
 FT TURN 105 105
 FT TURN 109 110
 FT STRAND 111 119
 FT STRAND 122 123
 FT TURN 124 125

Query Match 19.2% Score 418; DB 1; Length 277;
 Best Local Similarity 33.2%; Pred. No. 3e-28;

Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLVILSMPCGCHLIINNANFRESGLRTRTSGNIDCEKLRFRFSHFVWVKGLTA 209
 DB 34 DSNYSKMDYFENGGLGIIINNKNFKSTGTSRSGTVDAAKLRTRFRNKYEVRKNDLTR 93
 QY 210 KKMVLALAEARODHGA-LDCCVWILSHGCOASHLQFPGAVYDGCPSVKEKIVNIFNG 269
 DB 94 EEIVELMDVSKEDHSKRSSFCVLLSHGE-----GIIFGTNG-PVDLKKITNFRG 145
 QY 270 TSCPSLGGCKPKLFFIQACGGKQKHGFEVASTSPEDSPGNSPEPDATPQEGRLTFDQL 329
 DB 146 DRCSLTKGKPLFIQACRGTELDGCIETDSGVNDMM----- 182
 QY 330 DAISLPTSPDIFVSYSYTFPGFVSWRDPMKSGMYVETLDIFEOAHSEFQSLLLRVAN 389
 DB 183 -ACHKIPVDADFLVAYSTAPCYVSWRNSKDSWF:QSLCAMLKQYADKLEFMEHLTRVNR 241
 QY 390 AVSVK-----GIVKMPGCFNFKLFF 413
 DB 242 KVATEFESFSDATFHAKKQIPCVISMLTKELYF 275

RESULT 5

ICE3_MOUSE STANDARD; PRT: 277 AA.
 AC P70677; O08668; Q9QW14;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) [Cysteine protease CPP32] (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE).
 GN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3.";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
 RT activation of CPP32 in the apoptosis induced by a withdrawal of
 RT NGF.";
 RL Biochem. Biophys. Res. Commun. 231:770-774 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;

RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
 RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP--|--GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE
 CC CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.
 CC -!- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic
 CC TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,
 CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
 CC TESTIS.
 CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U54803; AAC52768.1;
 CC EMBL; U54802; AAC52768.1; JOINED.
 CC EMBL; U49929; AAC52764.1;
 CC EMBL; D86352; BAA2127.1;
 CC EMBL; Y13086; CAA73528.1;
 CC EMBL; U19522; AAC53196.1;
 CC EMBL; U63720; AAD09504.1;
 CC PIR; JC5410; JC5410.
 CC HSSP; P42574; 1PAU.
 CC MEROPS: C14.003;
 CC MGD; MGI:107239; Casp3
 CC InterPro; IPR002398; ICE.
 CC InterPro; IPR002138; ICE_p10.
 CC InterPro; IPR001309; ICE_p20.
 CC Pfam; PF00656; Peptidase C14; 1.
 CC PRINTS; PR00376; ILIBENZYM.
 CC SMART; SM00115; CASC; 1.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Zymog n; Apoptosis.
 CC PROPEP 1 9
 CC BY SIMILARITY.
 CC PROPEP 10 28
 CC CHAIN 29 175
 CC APOPAIN P17 SUBUNIT.
 CC CHAIN 176 277
 CC APOPAIN P12 SUBUNIT.


```
Matches 88; Conservative 52; Mismatches 92; Indels 42; Gaps 4;
QY 150 DLAYLSMEPGHCLINNNVFCRESGLRTTGS HICEKURRRFPSSLHFMVEYKGLTA 209
Db 34 DSSYNDYPMGLCIIINNFKHSTGMSARNG VTAANLRETFMALKYEVNRKNDLTR 93
QY 210 KKMVLALLEARQDHGALDCCVWVTLHGCGQASHLQI PGAVYGTGDCPVSVKEKIVNIFNG 269
Db 94 BEIMELMDSVKEDSKRSSFVCLVLSHGDE-----GVIPGTNG-PVDLKKLTSFFRG 145
QY 270 TSCPSLQKPKLPFTQACGQKDHGFVASTSPESPGSNPEPDATPFQEGRLTFDQL 329
Db 146 DYCRSLTGKPKLFTIACRGTELDGCIETDSTGDDDM----- 182
QY 330 DAISLPTPFDIVSYSTPFGVSWRDPKSSHWVETLDDIFEQWVHSEDLQSLLLRVAN 389
Db 183 -ACOKIPVEADFLVAYSTAPGYTSWRNSRDGSMFIQSLCAMLKLYAHKLEFMHILTRVR 241
QY 390 AVSVK-----GIYKMPGCFNFKLKKLF 413
Db 242 KVATEFESFSLDATFHAQKQIPCVISMLTKELYF 275

RESULT 8
ICE2_HUMAN STANDARD; PRT; 435 AA
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update.)
DE 15-SEP-2003 (Rel. 42, Last annotation update.)
DE Caspase-2 precursor (EC 3.4.22.2) (CASP-2) (ICH-1 protease) (ICH-
DE 1L/1S).
DE CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative
RL regulators of programmed cell death.";
RN Cell 78:739-750(1994).
RP [2]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shaham S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine
RT protease with substrate specificities similar to those of the human
RL Cpp32 protease.";
RL Genes Dev. 10:1073-1083(1996).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION C OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. M IT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR .L DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL.
CC -!- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ in the N- and C-termini;
CC Name=ICH-1L;
CC IsoId=p42575-1; Sequence=Displayed;
CC Note=Acts as a positive regulator of apoptosis;
CC Name=ICH-1S;
CC IsoId=p42575-2; Sequence=VSP 000801, SP 000802;
CC Note=Acts as a negative regulator of apoptosis;
CC TISSUE SPECIFICITY: EXPRESSED IN LARGE AMOUNTS IN THE EMBRYONIC
CC LUNG, LIVER AND KIDNEY THAN IN THE HEAR AND BRAIN. IN THE ADULTS
CC HIGHER LEVEL EXPRESSION IS SEEN IN THE PLACENTA, LUNG, KIDNEY,
CC PANCREAS THAN IN THE HEART, BRAIN, LIVER AND SKELETAL MUSCLE.
CC -!- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
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THAT OF OTHER CASPASES.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
-!- SIMILARITY: CONTAINS 1 CARD DOMAIN.

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EMBL: U13021; AAAS8959.1; -
EMBL: U13022; AAAS8960.1; -
PIR: A54821; A54821.
HSSP: P29466; 1ICE.
MEROPS: C14.006; -
Genew: HGNC:1503; CASP2.
MIM: 606639; -

GO: GO:0004202; F:caspase-2 activity; TAS.
GO: GO:0019899; F:enzyme binding activity; ISS.
GO: GO:0008632; P:apoptotic program; TAS.
GO: GO:0006508; P:proteolysis and peptidolysis; TAS.

InterPro: IPR001315; CARD.
InterPro: IPR002398; ICE.
InterPro: IPR002138; ICE_P10.
InterPro: IPR001309; ICE_P20.
Pfam: PF00619; CARD; 1.
Pfam: PF00656; Peptidase C14; 1.
PRINTS: PR00376; ILICENZYM.

SMART: SM00114; CARD; 1.
SMART: SM00115; CASC; 1.
PROSITE: PS0209; CARD; 1.
PROSITE: PS01122; CASPASE_CYS; 1.
PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS0207; CASPASE_P10; 1.
PROSITE: PS0208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.

PROPEP 1 152 CASPASE-2 SUBUNIT P18.
FT CHAIN 153 308
FT PROPEP 309 316 CASPASE-2 SUBUNIT P13.
FT CHAIN 317 435 CASPASE-2 SUBUNIT P12.
FT CHAIN 331 435 CARD.
FT DOMAIN 15 103 BY SIMILARITY.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 303 303 Missing (in isoform ICH-1S).
FT VARSPPLIC 1 14 /FTID=VSP 000801.

FT VARSPPLIC 306 435 DETDRGVQDCKNHAGSPGCEESDAGKEKLPKMLPRTSD
FT FT MITCGVACLKTAAMETKRGWYIEALAQVFERACDMHVA
FT FT DMLVKNALIKDREGYAPCTEPRCKEMSEYVSTLCRHLYL
FT FT FPGHPPT -> GGAIGSLGHLLEFLTAATASLAL (in
FT isoform ICH-1S).
FT /FTID=VSP 000802.
FT C->S: LOSS OF FUNCTION.
FT A->T: LOSS OF FUNCTION.
SQ SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FB7 CRC64;

Query Match 18.8%; Score 409; DB 1; Length 435;
Best Local Similarity 29.5%; Pred. No. 3.3e-27;
Matches 127; Conservative 66; Mismatches 155; Indels 82; Gaps 13;

QY 9 LRRCRLRVEELQVDLMDVLLSRELFRPHMEDIQ-BAGSSRRDQARQLIIDLETRGS 67

Db 23 LKKNRVLAQQLLELLEHLEKDIITLRELIQAKVGSFS-----QNVLELNLIPKRP 79

QY 68 QALPLFISCLEDTGQDMLASFLRTN-----RQAGKL 98

Db 80 QAFDAFCEALRETKOGHLEMLTLTSLGQHVLPPLSCDYLSLFPFVCSCLYKLR 139

QY 99 SKPTLENLT-----PVLIRPEIRKPEVLRPTPRVDIGSGFGVDGVALESIRGNADLAY 153

Db 140 STDITVEHSLDNKDPVCLO-----VKPCTP-----EFYQTHFOLEY 175

QY 154 ILSMEPCGCHLIINNVFCRESGLRTRTGSNIDCEKLRRLPSSILHFVYKGLDTAKQV 213
 Db 176 RLOSPRGALVLSNVHTGKELEFRSGGVDVSTLTVFKLLGYDVHVLCDOTAEMQ 235
 QY 214 LALLJELAR-QDHGALDCCVWVILSHGCOASHLQFPAGVYGTDCGCPVSEKIVNIFNGTSC 272
 Db 236 EKLNQFAQLPAHRVTDSCIVALLSHGVE-----GAIYGVYDGLKLLQEQVOLFQFNANC 288
 QY 273 PSLGKPKLFIQACGQKDHGEVASTSPEDSPGNSPEPDMTPQEGRLTFDQDAI 332
 Db 289 PSLQNKPKHFFIACRGDETDRGVDDQDGKXHGASPOCE-ESDA-----GKEKLPKX--- 339
 QY 333 SSLTPSPDIFVSYSTFPFGVSWRPKSGSWYVETLDDIFQWHAHSEDLQSLLLRVANAVS 392
 Db 340 -RLPTRSDMIGYACLKCTAAMRNTRKGSWYIEALQVFSERACDMHADVMLVKV-NAL- 396
 QY 393 VKGIYKQMPG 402
 Db 397 IKDRFGYAPG 406

RESULT 9
 CED3 CAEVU
 ID CED3 CAEVU STANDARD; PRT: 496 AA.
 AC P45436;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell death protein 3 precursor (EC 3.4.22.-).
 GN CED-3
 OS Caenorhabditis vulgaris.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Petoderinae; Caenorhabditis.
 OX NCBI_TaxID=31233;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94061982; PubMed=8242740;
 RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
 RT "The C. elegans cell death gene ced-3 encodes a protein similar to
 RT mammalian interleukin-1 beta-converting enzyme";
 RL Cell 75:641-652 (1993).
 CC -!- FUNCTION: ACTS AS A CYSTEINE PROTEASE. CONTROLLING PROGRAMMED
 CC CELL DEATH BY PROTEOLYTICALLY ACTIVATING OR INACTIVATING A
 CC SUBSTRATE PROTEIN OR PROTEINS. A POTENTIAL SUBSTRATE MAY BE CED-4.
 CC ALTERNATIVELY IT MIGHT DIRECTLY CAUSE CELL DEATH BY
 CC PROTEOLYTICALLY CLEAVING PROTEINS THAT ARE CRUCIAL FOR CELL
 CC VIABILITY (BY SIMILARITY).
 CC -!- SUBUNIT: COULD BE A HETERODIMER OF TWO SUBUNITS DERIVED FROM THE
 CC PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM.
 CC -!- PTM: MAY BE REGULATED BY PHOSPHORYLATION.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 DR HSP; P42574; ICP3.
 DR MEROPS; C14.002; .
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS02029; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
 KW CHAIN 1 364
 FT CELL DEATH PROTEIN 3 SUBUNIT 1
 FT (POTENTIAL).
 FT CHAIN 365 496
 FT CELL DEATH PROTEIN 3 SUBUNIT 2

FT DOMAIN 1 91
 FT ACT SITE 308 308 BY SIMILARITY.
 FT ACT SITE 351 351 BY SIMILARITY.
 SQ SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;
 Query Match 18.7%; Score 407; DB 1; Length 496;
 Best Local Similarity 24.5%; Pred. No. 5.8e-27;
 Matches 131; Conservative 74; Mismatches 159; Indels 170; Gaps 15;
 QY 1 MDEADRR-LLRRCRLRLVEELQVLDLWLLSRELFRPHMIEDIQRAGSG-----SRR 52
 Db 1 MMRQDRRLNERNILVFSNKLQSEQLDVLIAK-----DVLNSDNGDMINSCTER 51
 QY 53 DOARQLIIDLTRSQALPLFISCLEDTGQDMLASFLR-----THROAKLS 99
 Db 52 DKRKEQKAVQRRGDEAFDRFYDALRDTGHLLAAVLEPLATDLGCPMSPASHRRSALS 111
 QY 100 KPTLENLTPVVL-----RPEIRKPEVLRPET 125
 Db 112 PTFSSPTRVHRDSVSSVSTFYQDVYTRASTSRSSRLHTSDRHNYSNSRPSQ 171
 QY 126 PRPVDIGSGGFGDVGALES-----LRGNADLAYILSME----- 158
 Db 172 PSSANGSFTGCSGLGYSSSTRSYSKASAHSCYIFHEEDMNYVDAPTTHRVFDEKTMYN 231
 QY 159 ---PGHCLINNVNFCRESGLRTRTGSNIDCEKLRRLPSSILHFVYKGLDTAKQVLA 215
 Db 232 FSTPRGLCLIIINHEF---EQMPTRNGTKADKONLTNIFCMGYTVICKNIGORM-LT 287
 QY 216 LLELAROD-HGALDCCVWVILSHGCOASHLQFPAGVYGTDCGCPVSEKIVNIFNGTSCPS 274
 Db 288 IRDFAKNETHG--DSAILVILSHGEE-----NVIIGVDDVSNVHEIYDLLNANAPR 338
 QY 275 LGKPKLFFIACGGEQKDHGEVASTSPEDSPGNSPEPDMTPQEGRLTFDQDAISS 334
 Db 339 LANKPKLVFVQACRGERRDNGFPV-----LQSDVGVS 371
 QY 335 L-----PTSPDIFVSYSTFPFGVSWRPKSGSWYVET 366
 Db 372 LIRGDMNRDGNFGLGVRPQAGVWRKPKSQADILIRYATTAAQYVSWRNSARGSWFIOA 431
 QY 367 LDDIFEQWASEDLQSLLRVANAVS-----KGIYKMPGCGFNLKRLFF 413
 Db 432 VCEVFSTHAKMDVVELLTVNKKVACGFTQSOGANILKQMPENTSLRLKKFPYF 485

RESULT 10
 ICE8 MOUSE
 ID ICE8 MOUSE STANDARD; PRT: 480 AA.
 AC O89110; O35669;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-).
 GN CASP8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98316661; PubMed=9654089;
 RA Sakamaki K., Teukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8";
 RL Eur. J. Biochem. 253:399-405 (1998).
 RN 21
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=98057979; PubMed=9837723;
 RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
 RA van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
 RA Vandenabeele P.;

Molecular cloning and identification of murine caspase-8.;
 [3]
 J. Mol. Biol. 284:1017-1026(1998).
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heath N.K.,
 RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Prange T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Schaefer C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN SEQUENCE OF 57-476 FROM N.A.
 RP Kioschis P., Kischkel F., Poustka A., Kramer P.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Most upstream protease of the activation cascade of
 CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
 CC induced cell death. Binding to the adapter molecule FADD recruits
 CC it to either receptor. The resulting aggregate called death-
 CC inducing signaling complex (DISC) permits CASP8 proteolytic
 CC activation. The active dimeric enzyme is then liberated from the
 CC DISC and free to activate downstream apoptotic proteases.
 CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
 CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
 CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
 CC participate in the G2M8 apoptotic pathways. Cleaves APRT.
 CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
 CC Likely target for the coxsack virus CRMA death inhibitory protein.
 CC -1- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
 CC -1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
 CC Interacts with FADD and CFLAR (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
 CC Highest expression in spleen, thymus, lung, liver and kidney.
 CC Lower expression in heart, brain, testis and skeletal muscle.
 CC -1- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
 CC day 7.
 CC -1- PTM: Generation of the subunits requires association with the
 CC death-inducing signaling complex (DISC), whereas additional
 CC processing is likely due to the autocatalytic activity of the
 CC activated protease. G2MB and CASP10 can be involved in these
 CC processing events (By similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: AF067841; AAC40132.1;
 DR EMBL: AF067835; AAC40132.1; JOINED.
 DR EMBL: AF067836; AAC40132.1; JOINED.
 DR EMBL: AF067837; AAC40132.1; JOINED.
 DR EMBL: AF067838; AAC40132.1; JOINED.
 DR EMBL: AF067839; AAC40132.1; JOINED.
 DR EMBL: AF067840; AAC40132.1; JOINED.

DR EMBL: AF067834; AAC40131.1;
 DR EMBL: AJ007749; CAH07677.1;
 DR EMBL: BC006737; AAH06737.1;
 DR EMBL: AJ000641; CAA04196.1;
 DR HSSP: Q15806; IQOU.
 DR MEROPS: C14.009;
 DR MGD: MGI:1261423; Casp8
 DR GO: GO:0005737; Cytoplasm; IDA.
 DR GO: GO:0005634; Cnucleus; IDA.
 DR GO: GO:0004205; Fcaspase-8 activity; IDA.
 DR GO: GO:0006915; P:apoptosis; IDA.
 DR InterPro: IPR001875; DED.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF01335; DED; 2.
 DR Pfam: PF00656; Peptidase C14; 1.
 DR PRINTS: PRO0376; ILIBENZYM.
 DR SMART: SM00115; CASC; 1.
 DR SMART: SM00031; DED; 2.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS0207; CASPASE_P10; 1.
 DR PROSITE: PS0208; CASPASE_P20; 1.
 DR PROSITE: PS0168; DED; 2.
 DR Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat.
 FT PROPEP 1 218
 FT CHAIN 219 376
 FT PROPEP 377 387
 FT CHAIN 388 480
 FT ACT_SITE 319 319
 FT ACT_SITE 362 362
 FT DOMAIN 3 80
 FT DOMAIN 101 177
 FT CONFLICT 68 71
 FT CONFLICT 94 99
 FT CONFLICT 96 96
 FT CONFLICT 103 107
 FT CONFLICT 475 475
 SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5ED4F CRC64;
 Query Match 17.9%; Score 389.5; DB 1; Length 480;
 Best Local Similarity 28.5%; Pred. No. 1.7e-25;
 Matches 127; Conservative 66; Mismatches 159; Indels 93; Gaps 14;

QY 2 DEADRLRLRCRLRLVEELQVDQL--WDVLLSRLFRPHMIEDIQAGSGRRDQAROLI 59
 DB 94 DNAQISPYRVMLFKLSEEVSELELRSPKFLNNEIPKCKLEDCL-----SLLEIF 143
 QY 60 IDLETRGSQA---LPLFISCLDGTODMLASFLRTNROA--GKLSKPTLEML1-VVL-RP 113
 DB 144 VEMEKRTMLAENNLTKSIDQVKNLSLKGIEDYERSTERSMSELEGRELPSVLDEM 203
 QY 114 EIRKPEVLRPTPRPDVIGSGGFGDVGALESRLGNADLAYILSMPECGHCLIIINVPF-- 171
 DB 204 SLKMAELC--DSPREQD-----SESRSDKVVQMKPKRCYCLIIINHDFSK 248
 QY 172 CRES-----GLTRTGSNIDCEKLRRRESSLHFVVEVKGDLTAKMWLALLELARQDHGA 226
 DB 249 ARDITQLRKMKRGDKTDCDKEALSKTKFELHFEIVSYDDCTANEIHEILGYSADHKN 308
 QY 227 LDCCVVILSHGCAASHLQFPQAVYGTGCPVSVKEKVINFGTSCPSLGGKPKLFFIQA 286
 DB 309 KDCFCICCLSHGDK-----GVVYGTGKEASIDYLTSTYPTGSKCPSLSKPKIFFIQA 361
 QY 287 CGG-----EKQDHGFEVASTSPEDSPGNSPEPDATPFQEGRLTFDQDAIS 333
 DB 362 CGGNSFGKGVDFEAGFEQGHNT-EYDSSSHK-----N 393
 QY 334 SLPTSPDIFVSYSYTPFGVSMR1 PKSGSWYVETI--DDIFEQWANEHSDQLQSLLLVANVAS 392
 DB 394 YIPDEADFLGMATVKNCSYRDPVNGTWYIQLSQLSRKRCPOGDDILSLTGYNDVDS 453

AC Q9COK4; Q9UQ81;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
 DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
 DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
 DE CASP8 OR MCH5.
 GN Homo sapiens (Human).
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
 RC TISSUE=B-cell, and Thymus;
 RX MEDLINE=96279826; PubMed=8681376;
 RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;
 RT Involvement of MACH, a novel MORT1/FADD-interacting protease, in
 RT Fas/APO-1- and TNF receptor-induced cell death.";
 RL Cell 85:803-815(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
 RX MEDLINE=96279827; PubMed=8681377;
 RA Muzio M., Chinnaiyan A.M., Kischkel F.C., Gourde L.H., Schuler G.D.,
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
 RA Krammer P.H., Peter M.E., Dixit V.M.;
 RT FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
 RL Cell 85:817-827(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=T-cell;
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9913295; PubMed=9931493;
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
 RT "Structure and chromosome localization of the human CASP8 gene.";
 RL Gene 226:225-232(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=97373543; PubMed=9228018;
 RA Srinivasula S.M., Ahmad M., Oltie S., Bullrich F., Banks S.,
 RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
 RA Armering R.C., Alnemri E.S.;
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis.";
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21100893; PubMed=11161814;
 RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
 RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 RA Ikeda J.-E., Hayden M.R.;
 RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
 RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 RT critical region at chromosome 2q33-q34: Candidate genes for ALS2.";
 RL Genomics 71:200-213(2001).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
 RC TISSUE=Leukocyte;
 RX MEDLINE=22005982; PubMed=12010809;
 RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
 RA Harada M.;
 RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
 RT behaves as an inhibitor of the caspase cascade.";
 RL J. Cell Biol. 139:327-338(1997).
 RN [8]
 RP BLOOD 99:4070-4078(2002).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 7).
 RC TISSUE=Leukocyte;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marta M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=97121412; PubMed=8962078;
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
 RA Alnemri E.S.;
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
 RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
 RT Ced-3/ICE-like cysteine proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 RN [11]
 RP FUNCTION.
 RX MEDLINE=97160607; PubMed=9006941;
 RA Muzio M., Salvesen G.S., Dixit V.M.;
 RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
 RT zymogens.";
 RL J. Biol. Chem. 272:2952-2956(1997).
 RN [12]
 RP PROCESSING.
 RX MEDLINE=97372557; PubMed=9184224;
 RA Medina J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
 RA Krammer P.H., Peter M.E.;
 RT "FLICE is activated by association with the CD95 death-inducing
 RT signaling complex (DISC)."
 RL EMBO J. 16:2794-2804(1997).
 RN [13]
 RP CHARACTERIZATION OF ISOFORM 7.
 RX MEDLINE=20318377; PubMed=10860845;
 RA Horiuchi T., Himeji D., Tsukamoto H., Haraehima S., Hashimura C.,
 RA Hayashi K.;
 RT "Dominant expression of a novel splice variant of caspase-8 in human
 RT peripheral blood lymphocytes.";
 RL Biochem. Biophys. Res. Commun. 272:877-881(2000).
 RN [14]
 RP INTERACTION WITH BCL2; BCL2L1 AND BCAP31.
 RX MEDLINE=97477382; PubMed=9334338;
 RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
 RA Cromlish J.A., Shore G.C.;
 RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
 RT endoplasmic reticulum.";
 RL J. Cell Biol. 139:327-338(1997).


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DR InterPro; IPR002138; ICE_P10.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASP; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;
Query Match 16.7%; Score 364.5; DB 1; Length 303;
Best Local Similarity 33.7%; Pred No. 1.2e-23;
Matches 92; Conservative 40; Mismatches 96; Indels 43; Gaps 7;
QY 153 YILSMPCGCHLIINNVFCRESGLRTGNSIDCEKLRFRSLSHFVVKGLDTAKM 212
DB 60 YRMDFEKMKGKCIINNNKFNFKVTGMDVRNGTGDKAELFKCFRSLGDFDVFVYNDSCAKM 119
QY 213 VLALLELARODHGDCCVVVILSHGCCQASHLOFICAVYGTGDCPSVSEKIVNIENGTC 272
DB 120 QDLRKASEEDHSNACFACVLVSHGEE-----NLIVKDGVT-TPIKDLTAHFRGDR 171
QY 273 PSLGKPKLFFITQACGGEQKDHGFVASTSPEDSPGSPNPEPDATPFQEGRLTFDQDAI 332
DB 172 KTLLEKPKLFFITQACRGTELDGVQADS-----GPNETDANPRYK----- 212
QY 333 SSLPTSFDFVSYSFPGFVSRDRKSGSWYVETIDDIPEQWASGEDIQ--SLLLRVANA 390
DB 213 --IPVEADFLPAYSTVPGYVSRNPKGSGWVQA CSILDE--HGKDLIMQILTRVNRD 268
QY 391 VS-----VKGIYKQMPGCFNLRKLFF 13
DB 269 VARHFESQCDPCFNEKKQIPCMVSLTKELVF 101
RESULT 14
ICE7 HUMAN
ID ICE7_HUMAN STANDARD; PRT; 303 AA.
AC P55210; Q13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).
GN CASP7 OR MCH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RA Dixit V.M.;
RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
RT factor-induced apoptosis."
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RA Lippke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
RT cysteine protease similar to CPP32."

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RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandez-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,
RA Earnshaw W.C., Litwack G., Alnemri E.S.;
RT "Mch3, a novel human apoptotic cysteine protease highly related to
RT CPP32."
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
RC TISSUE=Fetal lung, and Fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandez-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of Cpp32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains."
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|GLY-217
CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.
CC -!- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=Alpha;
CC IsoId=P55210-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P55210-2; Sequence=VSP 000807;
CC Note=Not proteolytically active;
CC Name=Alpha';
CC IsoId=P55210-3; Sequence=VSP 000806;
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,
CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO
CC EXPRESSION IN THE BRAIN.

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CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4 AS BETA,
 CC BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED IT ALPHA'.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U39613; AAC50346.1; -
 CC EMBL; U40281; AAC50352.1; -
 CC EMBL; U37448; AAC50303.1; -
 CC EMBL; U37449; AAC50304.1; -
 CC EMBL; U67319; AAC51152.1; -
 CC EMBL; U67320; AAC51153.1; -
 CC EMBL; U67206; AAF21460.1; -
 CC EMBL; BC015799; AAH15799.1; -
 CC PDB; 1FIJ; 23-MAY-01.
 CC PDB; 1GQF; 04-JAN-02.
 CC PDB; 1I40; 31-OCT-01.
 CC PDB; 1I51; 23-FEB-02.
 CC PDB; 1K86; 21-NOV-01.
 CC PDB; 1K88; 21-NOV-01.
 CC PDB; 1KMC; 16-JAN-02.
 CC MEROPS; C14.004; -.
 CC Genew; HGNC:1508; CASP7.
 CC MIM; 601761; -.
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0008234; F-cysteine-type peptidase activity; TAS.
 CC GO; GO:0008632; P-apoptotic program; TAS.
 CC InterPro; IPR002398; ICE.
 CC InterPro; IPR021138; ICE_P10.
 CC InterPro; IPR001309; ICE_P20.
 CC Pfam; PF00656; Peptidase C14; 1.
 CC PRINTS; PR00376; IL1BCENZME.
 CC SMART; SM00115; CASc; 1.
 CC PROSITE; PS01122; CASPASE_C15; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
 KW 3D-structure. 1 23
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 FT CHAIN 24 198
 FT PROPEP 199 206
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT ACT_SITE 186 186
 FT VARSPIC 1 1 M -> MDCVGVPPGRKWHLEKNTSCGSSGICASYVTQM
 (in isoform Alpha').
 FT /FTID=VSP 000806.
 FT VARSPLIC 149 303
 FT VIYKGVTPPKDILTAHFRGDRCKTLLEKPKLFFIOACRG
 ELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGY
 SMRSPGRGSMFWCALCSILIEHGKOLEIMOILTRVNDVRAR
 HFESQSDDPHFHEK IOIPCVVSMILTKELYFESO -> MESCS
 VTQAGVQRDLGR JPPPRRLAEGPSLWASRPTRGPSMTQ
 MLILDRSQWKLKSSPIPRFQAITRGGAQAEGLCKPSA
 PSWRSTETKWKSCRSPG (in isoform Beta).
 FT /FTID=VSP 000807.
 FT MUTAGEN 186 186 C->A: NO APOPTOTIC ACTIVITY.
 FT CONFLICT 4 4 D -> E (IN REF. 5).
 FT CONFLICT 194 194 G -> A (IN REF. 1).
 FT SEQUENCE 303 AA; 34276 MW; CD37EB54A32CA4 CRC64;
 Query Match 16.6%; Score 361.5; DB 1; Length 303;

Best Local Similarity 33.3%; Pred. No. 2-2e-23;
 Matches 92; Conservative 41; Mismatches 94; Indels 49; Gaps 8;
 QY 153 YILSMPCGCHLIINNPNFCRESGLRTRTGSNTDCXLRKRRFSSLIHFMVEVKGLTAKOM 212
 DB 60 YNNMFKLGRKCIILNNKFNKDKVGMVNGTGDAAELKCFRSLGDFIVVNDSCAKM 119
 QY 213 VLALLEARODHGDALDCVVVILSHGCOASHLOFPGAVYGTDCGCVSVEKIVNFMGTSC 272
 DB 120 QDLKKAASEDHNAACFACILLSHGEE-----NVIYKGV-TPIKDLTAHFRGDR 171
 QY 273 PSLGKPKLFFIQACGGEQKHGFEVASTSPESGSPNPEPDATPFQEGRLTFDQDAI 332
 DB 172 KTLLEKPKLFFIQACRGTELDGQADS-----GPINDTDANPRYK----- 212
 QY 333 SSLPTPSDIFVSVSTFFGCVSWRDPKSGSWHYVTLLDIFEOWAHSEDLQ--SILLRVANA 390
 DB 213 --IPVADFLFAYSTVFGYYSWRSPGRGSMFWQALCSILEE--HGKDLIMQILTRVNR 268
 QY 391 VS-----VKGIVKQMPGCGFNFLRKLKLF 413
 DB 269 VARHFESGSDDDPHFHEK---KOIPCVVSMILTKELYF 301
 RESULT 15
 ICE7 MOUSE
 ID ICE7_MOUSE STANDARD; PRT; 303 AA.
 AC P97864; 008669;
 DT 01-NOV-1997 (Rel. 35. Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.) (LICE2 cysteine protease) (Apoptotic
 DE protease Mch-3).
 GN CASP7 OR MCH3 OR LICE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RX SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";
 RL Genomics 40:86-93(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97236307; PubMed=9125129;
 RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
 RA Momoi T.;
 RT "Mortmannin enhances CPP32-like activity during neuronal
 RT differentiation of P19 embryonal carcinoma cells induced by retinoic
 RT acid";
 RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenaabeele P., Declercq W., van der Brande I.,
 RA van Leeuwen M., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members";
 RL FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marta M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY)
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANTZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL c:station -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U67321; AAC53088.1; AUT_INIT.
DR EMBL; D86353; BAA19730.1; -
DR EMBL; Y13088; CAA73530.1; -
DR EMBL; BC005428; AAH05428.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004;
DR MGD; MGI:109383; Casp7.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASC.1
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23 BY SIMILARITY
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
FT CONFLICT 10 11 EL -> DW (IN REF. 2).
FT CONFLICT 45 45 A -> T (IN REF. 2).
FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
SQ SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;

Query Match 16.1%; Score 350.5; DB 1; Length 303;
Best Local Similarity 32.2%; Pred. No. 1.9e-22;
Matches 88; Conservative 42; Mismatches 100; Indels 43; Gaps 7;
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Db 60 YRMDFQRMGKCIINNNKFNFKATGMDVNRNGTDKAGALFKCFQNLGFEVTVHNDSCAKM 119
QY 213 VLALLELARODHGALDCVVVVILSHGCOASHLQPPGAVYGTDCGCVSVEKIVNIFNGTSC 272
Db 120 QDLURKASEEDHNSACFACVLLSHGEE-----DLIYKQGV-TPIKDLTAHFRGDR 171
QY 273 PSLGKPKLFFIOACGGEQKHGFVASTSPEDSPGSPNPEDATPFQEGRLTFDQDAI 332
Db 172 KTLLEKPKLFFIOACRGTELDGIGQADS-----GPINDIDANP-----R 210
QY 333 SSLPTSPDIFVSYSTPFGFVSWRDPKSGSWVETLDDIFQWAHSEDLQ--SELLRVANA 390
Db 211 NKIPVEADFLFAYSTVPGYYSWRNPGKSWFVQALCSILNE--HGKOLEIMQILTRVNR 268
QY 391 VSVK-----GIYKQMPGCFNFKLKLFF 413
Db 269 VARHFESQSDDPRENEKKQIPCMVSMLTKEYLF 301

Search completed: October 20, 2003, 12:11:40
Job time : 26 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: October 20, 2003, 12:13:31 ; Search time 69 Seconds
 (without alignments)
 988.254 Million cell updates/sec

Title: US-09-961-201a-1
 Perfect score: 2180
 Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKQMPCCFNLRKLLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 609560 seqs, 163917102 residues

Total number of hits satisfying chosen parameters 609560

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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 2: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:
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 15: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:
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 18: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2166	99.4	416	US-10-068-569-1	Sequence 1, Appli
2	2157	98.9	416	US-09-954-697-30	Sequence 30, Appl
3	2153	98.8	416	US-09-851-873-102	Sequence 102, App
4	2153	98.8	416	US-10-141-618-4	Sequence 4, Appli
5	2153	98.8	416	US-10-059-749-2	Sequence 2, Appli
6	468	21.5	93	US-10-314-507-27	Sequence 27, Appl
7	468	21.5	93	US-10-014-26-27	Sequence 27, Appl
8	468	21.5	93	US-10-002-974-27	Sequence 27, Appl
9	418	19.2	264	US-10-103-448-3	Sequence 3, Appli
10	418	19.2	264	US-10-108-929-3	Sequence 3, Appli
11	418	19.2	277	US-09-895-263-4	Sequence 4, Appli
12	418	19.2	277	US-09-954-697-12	Sequence 12, Appl
13	418	19.2	277	US-09-851-873-98	Sequence 98, Appl
14	418	19.2	277	US-10-280-670-5	Sequence 5, Appli
15	418	19.2	277	US-10-214-932-108	Sequence 108, App

16	418	19.2	277	15	US-10-207-655-202	Sequence 202, App
17	414	19.0	452	12	US-10-205-219-52	Sequence 52, Appl
18	409.5	18.8	451	10	US-09-888-243-28	Sequence 28, Appl
19	409	18.8	435	8	US-08-459-455-51	Sequence 51, Appl
20	409	18.8	435	10	US-09-954-697-9	Sequence 9, Appli
21	409	18.8	435	12	US-09-851-873-97	Sequence 97, Appl
22	409	18.8	435	12	US-10-280-670-9	Sequence 9, Appli
23	409	18.8	441	8	US-08-459-455-43	Sequence 43, Appl
24	401.5	18.4	505	10	US-09-888-243-5	Sequence 5, Appli
25	395.5	18.1	503	8	US-08-459-455-36	Sequence 36, Appl
26	395.5	18.1	503	15	US-10-123-529-8	Sequence 8, Appli
27	385.5	17.7	503	10	US-08-459-455-2	Sequence 2, Appli
28	385.5	17.7	503	10	US-09-888-243-29	Sequence 29, Appl
29	385.5	17.7	503	12	US-10-280-670-10	Sequence 10, Appl
30	383	17.6	479	9	US-09-410-194-20	Sequence 20, Appl
31	383	17.6	479	12	US-09-851-873-101	Sequence 101, App
32	382.5	17.5	497	15	US-10-123-529-9	Sequence 9, Appli
33	382	17.5	496	9	US-09-952-768-4	Sequence 4, Appli
34	378.5	17.4	503	8	US-08-459-455-35	Sequence 35, Appl
35	378.5	17.4	503	15	US-10-123-529-7	Sequence 7, Appli
36	378	17.3	286	9	US-08-862-915-1	Sequence 1, Appli
37	377.5	17.3	497	8	US-08-459-455-37	Sequence 37, Appl
38	376.5	17.3	476	10	US-09-954-697-27	Sequence 27, Appl
39	371.5	17.0	478	11	US-09-009-893-3	Sequence 3, Appli
40	363.5	16.7	479	10	US-09-888-243-6	Sequence 6, Appli
41	361.5	16.6	303	10	US-09-944-851-2	Sequence 2, Appli
42	361.5	16.6	303	10	US-09-954-697-24	Sequence 24, Appl
43	361.5	16.6	303	12	US-09-851-873-100	Sequence 100, App
44	361.5	16.6	303	12	US-10-280-670-4	Sequence 4, Appli
45	361.5	16.6	303	15	US-10-337-060-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-10-068-569-1
 ; Sequence 1, Application US/10068569
 ; Publication No. US20020160975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Srinivasula, Srinivasa M.
 ; APPLICANT: Fernandes-Alnemri, Teresa
 ; APPLICANT: Alnemri, Emad S.
 ; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
 ; FILE REFERENCE: 480140.475
 ; CURRENT APPLICATION NUMBER: US/10/068.569
 ; CURRENT FILING DATE: 2002-02-06
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 416
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-068-569-1

Query Match	99.4%	Score	2166	DB	14	Length	416
Best Local Similarity	99.3%	Pred. No.	8e-207				
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Gaps	0						
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Qy 361 SWVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416
Db 361 SWVETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKOMPFCFNLKRLFFKTS 416

RESULT 2
US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemtil, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.43102
; CURRENT APPLICATION NUMBER: US/09/954,697
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-697-30

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Best Local Similarity 99.0%; Pred. No. 6 3e-206;
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RESULT 3
US-09-851-873-102
; Sequence 102, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:

; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-102

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Best Local Similarity 98.8%; Pred. No. 1.6e-205;
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RESULT 4
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-4

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Best Local Similarity 98.8%; Pred. No. 1.6e-205;
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Db 181 TGSNIDCEKLRRLRRFSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVVILSHGCG 240
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RESULT 5
US-10-059-749-2
; Sequence 2, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;      Fernandes-Alnemri, Teresa
;      Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4170 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-059-749-2
```

```
Query Match      98.8%; Score 2153; DB 14; Length 416;
Best Local Similarity 98.8%; Pred. No. 1.6e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDDAARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDDAARQLII 60
Qy 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPEPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLIIINNPNFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCLIIINNPNFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRFSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRRLRRFSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVVILSHGCG 240
Qy 241 ASHLQFPFVAVGTGDCPVSVVEKIIVNFGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPFVAVGTGDCPVSVVEKIIVNFGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
Qy 301 TSPEDESPGSPNPEDATPFQGLRTFDQLDAISSLTPSDIFVSYSTFFGFSWRDPKSG 360
Db 301 TSPEDESPGSPNPEDATPFQGLRTFDQLDAISSLTPSDIFVSYSTFFGFSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWHAHSEDQLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWHAHSEDQLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 6
US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-314-506-27

Query Match      21.5%; Score 468; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 9.5e-39;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDDAARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDDAARQLII 60
Qy 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNR 93
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Db 61 DLETRGSQLPLFISCLDGTQDMCLASFLRTNR 93

RESULT 7

US-10-014-269-27

Sequence 27, Application US/10014269

Publication No. US20020127673A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

APPLICANT: Oguri, Yasunori

TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins

FILE REFERENCE: UM-06645

CURRENT APPLICATION NUMBER: US/10/014,269

CURRENT FILING DATE: 2001-10-26

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 93

TYPE: PRT

ORGANISM: Homo sapiens

US-10-014-269-27

Query Match 21.5%; Score 468; DB 14; Length 93;

Best Local Similarity 100.0%; Pred. No. 9.5e-39;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDLVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEELQVDQLWDLVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60

QY 61 DLETRGSQLPLFISCLDGTQDMCLASFLRTNR 93

Db 61 DLETRGSQLPLFISCLDGTQDMCLASFLRTNR 93

RESULT 8

US-10-002-974-27

Sequence 27, Application US/10002974

Publication No. US20020197616A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Oguri, Yasunori

APPLICANT: Cho, Judy

APPLICANT: Niccolae, Dan L

APPLICANT: Bonen, Denise

TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins

FILE REFERENCE: UM-06646

CURRENT APPLICATION NUMBER: US/10/002,974

CURRENT FILING DATE: 2001-10-26

NUMBER OF SEQ ID NOS: 99

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 93

TYPE: PRT

ORGANISM: Homo sapiens

US-10-002-974-27

Query Match 21.5%; Score 468; DB 14; Length 93;

Best Local Similarity 100.0%; Pred. No. 9.5e-39;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDLVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEELQVDQLWDLVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60

QY 61 DLETRGSQLPLFISCLDGTQDMCLASFLRTNR 93

Db 61 DLETRGSQLPLFISCLDGTQDMCLASFLRTNR 93

RESULT 9

US-10-103-448-3

Sequence 3, Application US/10103448

Publication No. US20020155579A1

GENERAL INFORMATION:

APPLICANT: Krebs, Joseph F.

APPLICANT: Srinivasan, Anu

APPLICANT: Fritz, Lawrence C.

APPLICANT: Wu, Joseph C.

TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS

FILE REFERENCE: 480140.468D1

CURRENT APPLICATION NUMBER: US/10/103,448

CURRENT FILING DATE: 2002-03-20

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 264

TYPE: PRT

ORGANISM: Homo sapien

US-10-103-448-3

Query Match 19.2%; Score 418; DB 14; Length 264;

Best Local Similarity 33.2%; Pred. No. 4.3e-33;

Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPEPCGHCLIIINNVCRESGLRTRTGSNIDCEKLRRRFSSLHFVYVKGDLTA 209

Db 21 DNSYKMDYPEMGLCIIINNKNFKSTGRTSRSGTDVDAANLRETERNLKYEVRNKNLUTR 80

QY 210 KKWVLALLELARQDHGALDCCVVVILSHGCCQASHLQFPGVYVGTGDCPVSVEKIVNIENG 269

Db 81 EEIVELMRDVSKEDEHSKSSSFVCLLSHCEE-----GIIFGTNG-PVDLKKITNFRG 132

QY 270 TSCPSLGGKPKLFFIOACGGEQKHGFVASTSPEDSPGSPNPEDATPFQEGLRTFQOL 329

Db 133 DRCRLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 169

QY 330 DAISLPTSDJFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLOSLLLRVAN 389

Db 170 -ACHKIPVDADELYAYSTAGVYSWRNSKGSWFTQSLCAMLKQYADKLEFMHILTVNR 228

QY 390 AVSVK-----GIYKMPGCFNFKLFF 413

Db 229 KVATEFESFSDATTHAKKQIPIVSMILTKELYF 262

RESULT 10

US-10-108-929-3

Sequence 3, Application US/10108929

Publication No. US20020197702A1

GENERAL INFORMATION:

APPLICANT: Krebs, Joseph F.

APPLICANT: Srinivasan, Anu

APPLICANT: Fritz, Lawrence C.

APPLICANT: Wu, Joseph C.

TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS

FILE REFERENCE: 480140.468D2

CURRENT APPLICATION NUMBER: US/10/108,929

CURRENT FILING DATE: 2002-03-26

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 264

TYPE: PRT

ORGANISM: Homo sapien

US-10-108-929-3

Query Match 19.2%; Score 418; DB 14; Length 264;

Best Local Similarity 33.2%; Pred. No. 4.3e-33;

Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPEPCGHCLIIINNVCRESGLRTRTGSNIDCEKLRRRFSSLHFVYVKGDLTA 209

Db 21 DLSYKMDYPEMGLCIIINNNFKHSTGTSRSGTDVDAANLRETRNLKYEVRNKDLTR 80
Qy 210 KMWYLLALLEARQDHGALDCCVVWILSHGCOASHLQFPCAVYGTGDCPVSVKEKIVNIENG 269
Db 81 EEIVELMRDVSKEHSHKSSRFFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFRFG 145
Qy 270 TSCPSLGKPKLFFIOACGGEQKHGFVASTSPEDSPGSNPEPDATPFQEGRLTFDOL 329
Db 133 DRCRLTGKPKLFIQACRGTELDGCIETDGVDDM----- 182
Qy 330 DAISLPTSPDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVAN 389
Db 170 -ACHKIPVDADEFLAYSTAGPYYSWRNSKDSWFIQSLCAMLKQYADKLEFHMILTRVNR 241
Qy 390 AVSVK-----GIYKQMPGCFNFKLFF 413
Db 229 KVATEFESFSDATFHAKKQIPCIIVSMULTKELYF 275

RESULT 11

US-09-895-263-4
; Sequence 4, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,263
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF140
; TELEPHONE: 301-251-6015
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-895-263-4
Query Match 19.2%, Score 418; DB 9; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.7e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
Qy 150 DLAYLSMEPCGHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVMEVKGDLTA 209
Db 34 DLSYKMDYPEMGLCIIINNNFKHSTGTSRSGTDVDAANLRETRNLKYEVRNKDLTR 93

Qy 210 KMWYLLALLEARQDHGALDCCVVWILSHGCOASHLQFPCAVYGTGDCPVSVKEKIVNIENG 269
Db 94 EEIVELMRDVSKEHSHKSSRFFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFRFG 145
Qy 270 TSCPSLGKPKLFFIOACGGEQKHGFVASTSPEDSPGSNPEPDATPFQEGRLTFDOL 329
Db 146 DRCRLTGKPKLFIQACRGTELDGCIETDGVDDM----- 182
Qy 330 DAISLPTSPDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVAN 389
Db 183 -ACHKIPVDADEFLAYSTAGPYYSWRNSKDSWFIQSLCAMLKQYADKLEFHMILTRVNR 241
Qy 390 AVSVK-----GIYKQMPGCFNFKLFF 413
Db 242 KVATEFESFSDATFHAKKQIPCIIVSMULTKELYF 275

RESULT 12

US-09-954-697-12
; Sequence 12, Application US/09954697
; Patent No. US2002010631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 277
; TYPE: PRP
; ORGANISM: Homo sapien
; US-09-954-697-12

Query Match 19.2%, Score 418; DB 10; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.7e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

Qy 150 DLAYLSMEPCGHCLIIINNVNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVMEVKGDLTA 209
Db 34 DLSYKMDYPEMGLCIIINNNFKHSTGTSRSGTDVDAANLRETRNLKYEVRNKDLTR 93
Qy 210 KMWYLLALLEARQDHGALDCCVVWILSHGCOASHLQFPCAVYGTGDCPVSVKEKIVNIENG 269
Db 94 EEIVELMRDVSKEHSHKSSRFFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFRFG 145
Qy 270 TSCPSLGKPKLFFIOACGGEQKHGFVASTSPEDSPGSNPEPDATPFQEGRLTFDOL 329
Db 146 DRCRLTGKPKLFIQACRGTELDGCIETDGVDDM----- 182
Qy 330 DAISLPTSPDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLLRVAN 389
Db 183 -ACHKIPVDADEFLAYSTAGPYYSWRNSKDSWFIQSLCAMLKQYADKLEFHMILTRVNR 241
Qy 390 AVSVK-----GIYKQMPGCFNFKLFF 413
Db 242 KVATEFESFSDATFHAKKQIPCIIVSMULTKELYF 275

RESULT 13

US-09-851-873-98
; Sequence 98, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Irene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08

; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-98

Query Match 19.2%; Score 418; DB 12; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.7e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRFSSLHFMVEVKGDLTA 209
DB 34 DNSYKMDYPEMGLCIIINNNFKHSTGTSRSGTDVAANLRETFRNLYKEVRNKNDLTR 93
QY 210 KKMVLALLELARODHGALDCCVVVILSHGQASHLOFPGAVYGTGDCPSVSEKIVNIFNG 269
DB 94 EEIVELMRDVSKEHDSKRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145
QY 270 TSCPSLGGKPKLFIQACGGEQKHGFVASTSPEDSPGSPNPEPDATPFQEGRLTFDQL 329
DB 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182
QY 330 DAISSLTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSQLLRVAN 389
DB 183 -ACHKIPVDADFLYAYSTAGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFPHILTRVNR 241
QY 390 AVSVK-----GIYKQMPGCFNFKKLF 413
DB 242 KVATEFESFSDATFHAKKQIPICIVSMLTKELYF 275

RESULT 14
US-10-280-670-5
; Sequence 5, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-5

Query Match 19.2%; Score 418; DB 12; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.7e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRFSSLHFMVEVKGDLTA 209
DB 34 DNSYKMDYPEMGLCIIINNNFKHSTGTSRSGTDVAANLRETFRNLYKEVRNKNDLTR 93
QY 210 KKMVLALLELARODHGALDCCVVVILSHGQASHLOFPGAVYGTGDCPSVSEKIVNIFNG 269
DB 94 EEIVELMRDVSKEHDSKRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145
QY 270 TSCPSLGGKPKLFIQACGGEQKHGFVASTSPEDSPGSPNPEPDATPFQEGRLTFDQL 329
DB 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSG----- 182
QY 330 DAISSLTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSQLLRVAN 389

DB 183 -ACHKIPVDADFLYAYSTAGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFPHILTRVNR 241
QY 390 AVSVK-----GIYKQMPGCFNFKKLF 413
DB 242 KVATEFESFSDATFHAKKQIPICIVSMLTKELYF 275

RESULT 15
US-10-214-932-108
; Sequence 108, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION:
; APPLICANT: HWANG, Inhwan
; APPLICANT: KIM, Dae Heon
; APPLICANT: LEE, Yong Jik
; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
; FILE REFERENCE: APB02/US
; CURRENT APPLICATION NUMBER: US/10/214,932
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-214-932-108

Query Match 19.2%; Score 418; DB 15; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.7e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRFSSLHFMVEVKGDLTA 209
DB 34 DNSYKMDYPEMGLCIIINNNFKHSTGTSRSGTDVAANLRETFRNLYKEVRNKNDLTR 93
QY 210 KKMVLALLELARODHGALDCCVVVILSHGQASHLOFPGAVYGTGDCPSVSEKIVNIFNG 269
DB 94 EEIVELMRDVSKEHDSKRSSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145
QY 270 TSCPSLGGKPKLFIQACGGEQKHGFVASTSPEDSPGSPNPEPDATPFQEGRLTFDQL 329
DB 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182
QY 330 DAISSLTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSQLLRVAN 389
DB 183 -ACHKIPVDADFLYAYSTAGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFPHILTRVNR 241
QY 390 AVSVK-----GIYKQMPGCFNFKKLF 413
DB 242 KVATEFESFSDATFHAKKQIPICIVSMLTKELYF 275

Search completed: October 20, 2003, 12:23:18
Job time : 71 secs

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OM protein - protein search, using sw model

Run on: October 20, 2003, 12:14:57 ; Search time 23 Seconds
(without alignments)
850.570 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 416

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNRLKLPFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : C

Total number of hits satisfying chosen parameter is: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219	52.6	416	1 ICE9 HUMAN	P52211 homo sapien
2	11	2.6	299	1 ICE1 SPOPR	P89116 spodoptera
3	11	2.6	323	1 ICE1 DROME	O02002 drosophila
4	11	2.6	339	1 ICE DROME	O01382 drosophila
5	10	2.4	303	1 ICE7 HUMAN	P55210 homo sapien
6	10	2.4	303	1 ICE7 MESAU	P55214 mesocricetu
7	10	2.4	303	1 ICE7 MOUSE	P97864 mus musculus
8	10	2.4	521	1 ICEA HUMAN	Q92851 homo sapien
9	9	2.2	484	1 CELA MOUSE	O35732 m casp8 and
10	9	2.2	1196	1 BR11 ARATH	O22476 arabidopsis
11	8	1.9	232	1 YK10 ARCFU	O28269 archaeoglob
12	8	1.9	579	1 Y876 MYCLE	O33057 mycobacteri
13	8	1.9	1207	1 BR11 LYCES	Q98uqs lycopersico
14	8	1.9	1207	1 BR11 LYCPE	Q81899 lycopersico
15	8	1.9	1393	1 RPOC CHLPN	Q92999 chlamydia p
16	7	1.7	132	1 GCSH MYCLE	O32920 mycobacteri
17	7	1.7	180	1 PTH CHLPN	Q926v6 chlamydia p
18	7	1.7	196	1 HNK2 XENLA	P42587 xenopus lae
19	7	1.7	210	1 GDB RHILLO	Q98d22 rhizobium l
20	7	1.7	264	1 R3B RALSO	Q8xv18 ralsstonia s
21	7	1.7	274	1 NNS STRAS	P52391 streptomyces
22	7	1.7	306	1 SOSB PSES9	P52686 pseudomonas
23	7	1.7	338	1 G3P THEVO	Q97bJ8 thermoplasm
24	7	1.7	345	1 TRPD AERPE	Q9y8t2 aeropyrum p
25	7	1.7	401	1 RAL7 YEAST	P48581 saccharomyc
26	7	1.7	404	1 YBR3 YEAST	P38083 saccharomyc
27	7	1.7	420	1 BACA RHIME	Q98120 rhizobium m
28	7	1.7	442	1 IFR2 HUMAN	Q12894 homo sapien
29	7	1.7	480	1 ICE8 MOUSE	O89110 mus musculus
30	7	1.7	487	1 PHOQ SALTJ	P14147 salmonella
31	7	1.7	504	1 PSD5 HUMAN	Q16401 homo sapien
32	7	1.7	505	1 SPKD SYN3	P54735 synechocyst
33	7	1.7	548	1 SYX HALN1	Q9hnn7 halobacteri

34	7	1.7	551	1 E2K2 HUMAN	P19525 homo sapien
35	7	1.7	575	1 GGT PSESP	P36267 pseudomonas
36	7	1.7	628	1 LU HUMAN	P50895 homo sapien
37	7	1.7	664	1 UL47 HSV1F	P08313 herpes simp
38	7	1.7	749	1 TR2M AGRRH	Q09109 agrobacteri
39	7	1.7	755	1 TR2M AGRT4	P04029 agrobacteri
40	7	1.7	755	1 TR2N AGRT4	P25017 agrobacteri
41	7	1.7	778	1 YQ34 MYCTU	P71933 mycobacteri
42	7	1.7	1011	1 CAPP SYNEL	Q94gb2 synechococ
43	7	1.7	1062	1 UL70 HCMVA	P17149 human cytom
44	7	1.7	1507	1 Y056 HUMAN	P42695 homo sapien
45	7	1.7	1597	1 OTOF HUMAN	Q98c10 homo sapien
46	7	1.7	3119	1 CAIC MOUSE	Q60847 mus musculu
47	7	1.7	3259	1 GIAN HUMAN	Q14789 homo sapien
48	6	1.4	45	1 AT12 HSVE4	Q00041 equine herp
49	6	1.4	67	1 GON1 MACMU	P55247 macaca mula
50	6	1.4	71	1 YOKK BACSU	P54573 bacillus au
51	6	1.4	75	1 RL29 MYCBO	O06050 mycobacteri
52	6	1.4	84	1 NTXP TITSE	O77463 tityus seir
53	6	1.4	84	1 SCX7 TITBA	P56611 tityus bahr
54	6	1.4	84	1 SCX7 TITSE	P15226 tityus serr
55	6	1.4	84	1 SCX7 TITST	P56612 tityus stig
56	6	1.4	87	1 Y32A MYCGE	Q92b75 mycoplasma
57	6	1.4	89	1 SLTB BPH30	P08027 bacterioph
58	6	1.4	90	1 GON1 MOUSE	P13562 mus musculu
59	6	1.4	91	1 GON1 PIG	P49921 sus scrofa
60	6	1.4	92	1 GON1 CAVPO	O54713 cavia porce
61	6	1.4	92	1 GON1 HUMAN	P01148 homo sapien
62	6	1.4	92	1 GON1 TUPGB	Q95335 tupaia glis
63	6	1.4	95	1 IHFB RHOCA	Q06607 rhodobacter
64	6	1.4	97	1 PY D1CLA	Q96t98 dicentrarch
65	6	1.4	98	1 ACTO HUMAN	P07311 homo sapien
66	6	1.4	98	1 ACYO MOUSE	P56376 mus musculu
67	6	1.4	100	1 ACYO PIG	P24540 sus scrofa
68	6	1.4	104	1 RS17 THETH	P24321 thermus the
69	6	1.4	110	1 ETS2 LYTVA	P29773 lytechinus
70	6	1.4	110	1 INS RABIT	P01311 oryctolagus
71	6	1.4	111	1 TMOC PSEME	Q00458 pseudomonas
72	6	1.4	112	1 THL CLODI	P45362 clostridium
73	6	1.4	115	1 RL19 BUCAI	P57477 buchnera ap
74	6	1.4	115	1 RL19 BUCAP	Q8k9f3 buchnera ap
75	6	1.4	115	1 VG52 HSVSA	Q01050 herpesvirus

ALIGNMENTS

RESULT 1	
ICE9 HUMAN	STANDARD: PRT: 416 AA.
ID ICE9 HUMAN	Q98062; Q9UEQ3; Q9UIJ8;
AC P55211: Q95348; Q92852; Q98062; Q9UEQ3; Q9UIJ8;	
DT 01-OCT-1996 (Rel. 34, Created)	
DT 28-FEB-2003 (Rel. 41, Last sequence update)	
DT 15-SEP-2003 (Rel. 42, Last annotation update)	
DE Caspase-9 precursor (BC 3.4.22.-) (CASP-9) (ICE-like apoptotic	
DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease	
DE activating factor 3) (APAF-3).	
GN CASP9 OR MCH6.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.	
RX MEDLINE:96279246; PubMed:8663294;	
RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,	
RA He W.-W., Dixit V.M.;	
RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated	
RT by the cytotoxic T cell protease granzyme B.";	
RL J. Biol. Chem. 271:16720-16724(1996).	
[2]	
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.	
RN TISSUE=T-cell;	

RX MEDLINE=97059171; PubMed=8900201;
 RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
 RA Alnemri R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.,
 RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
 RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
 RT mediator CPP32.";
 RL J. Biol. Chem. 271:27099-27106(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99315341; PubMed=10384055;
 RA Hadano S., Nahir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
 RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.,
 RT "Genomic organization of the human caspase-9 gene on chromosome
 RT 1p36.1-p36.3.";
 RL Mamm. Genome 10:757-760(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99168502; PubMed=10070954;
 RA Srinivasula S.M., Almad M., Guo Y., Zhan Y., Lazebnik Y.,
 RA Fernandes-Alnemri T., Alnemri E.S.,
 RT "Identification of an endogenous dominant-negative short isoform of
 RT caspase-9 that can regulate apoptosis.";
 RL Cancer Res. 59:999-1002(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Stomach cancer;
 RA Izawa M., Mori T., Ito H., Sairenji T.,
 RT "Molecular cloning and sequencing of a cDNA predicting an alternative
 RT form of pro-caspase-9 from human gastric cancer cell lines.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Miho Y., Momoi T., Fujita E.,
 RT "A novel splicing product of human caspase-9 lacking protease
 RT activity.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-28.
 RX MEDLINE=99107856; PubMed=9890966;
 RA Seol D.W., Billiar T.R.,
 RT "A caspase-9 variant missing the catalytic site is an endogenous
 RT inhibitor of apoptosis.";
 RL J. Biol. Chem. 274:2072-2076(1999).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28; LEU-99; ILE-102;
 RP VAL-106; ASP-114; HIS-173 AND ARG-221.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Fel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.J., Nickerson D.A.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Thomas D.,
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Eye, and Lymph;
 RX MEDLINE=22188257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Slaughter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Savant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Baha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Matek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
 RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 TO APAF-
 CC 1 LEADS TO ACTIVATION OF THE PROTEASE WHICH THEN CLEAVES AND
 CC ACTIVATES CASPASE-3. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE)
 CC POLYMERASE (PARP).
 CC -i- FUNCTION: Isoform 2 lacks activity is an dominant-negative
 CC inhibitor of caspase-9.
 CC -i- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.
 CC Caspase-9 and APAF1 bind to each other via their respective NH2-
 CC terminal CED-3 homologous domains in the presence of cytochrome C
 CC and ATP. Interacts with BIRC7.
 CC -i- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=9L, Alpha;
 CC IsoId=P55211-1; Sequence=Displayed;
 CC Name=2; Synonyms=9S, Beta;
 CC IsoId=P55211-2; Sequence=VSP_000818;
 CC -i- TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHEST EXPRESSION IN THE
 CC HEART, MODERATE EXPRESSION IN LIVER, SKELETAL MUSCLE, AND
 CC PANCREAS. LOW LEVELS IN ALL OTHER TISSUES.
 CC -i- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
 CC GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE
 CC INVOLVED IN THESE PROCESSING EVENTS.
 CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -i- SIMILARITY: Contains 1 CARD domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; U56390; AAC50640.1; -;
 DR EMBL; U60521; AAC50776.1; -;
 DR EMBL; AB019205; BAA82697.1; -;
 DR EMBL; AB019197; BAA82697.1; JOINED.
 DR EMBL; AB019198; BAA82697.1; JOINED.
 DR EMBL; AB019199; BAA82697.1; JOINED.
 DR EMBL; AB019200; BAA82697.1; JOINED.
 DR EMBL; AB019201; BAA82697.1; JOINED.
 DR EMBL; AB019202; BAA82697.1; JOINED.
 DR EMBL; AB019203; BAA82697.1; JOINED.
 DR EMBL; AB019204; BAA82697.1; JOINED.
 DR EMBL; AF093130; AAD12248.1; -;
 DR EMBL; AB015653; BAA78780.1; -;
 DR EMBL; AB020979; BAA87905.1; -;
 DR EMBL; AF110376; AAD13615.1; -;
 DR EMBL; AL512883; CAC42423.1; -;
 DR EMBL; AY214168; AAO21133.1; -;
 DR EMBL; BC002452; AAH02452.1; -;
 DR EMBL; BC006463; AAH06463.1; -;
 DR PDB; 3YGS; 19-APR-00.
 DR MEROPS; C14.010; -;
 DR Genew; HGNC:1511; CASP9.
 DR MIM; 602234; -;
 DR GO; GO:004211; F:caspase-9 activity; TAS.
 DR GO; GO:0008047; F:enzyme activator activity; TAS.
 DR GO; GO:0008632; P:apoptotic program; TAS.
 DR GO; GO:0008635; P:caspase activation via cytochrome c; TAS.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR001309; ICE_p10.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00656; Peptidase_C14; 1.

RC TISSUE=Embryo;
RX MEDLINE=97153052; PubMed=899799;
RA Song Z., McCall K., Steller H.;
RT "DCP-1, a Drosophila cell death protease essential for development.";
RL Science 275:536-540(1997).
RN [2]
RP ERRATUM.
RA Song Z., McCall K., Steller H.;
RL Science 277:167-167(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu C., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rochia S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Stadler A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasearman D.A., Weinstock G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zheng G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY).
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). LOSS
CC OF CYCLOTIC DCP-1 FUNCTION CAUSES LARVAL LETHALITY AND MELANOTIC
CC TUMORS.
CC -!- SUBUNIT: HETERODIMER OF A 22 kDa (P22) AND A 13 kDa (P13) SUBUNIT.
CC -!- DEVELOPMENTAL STAGE: PRESENT UNIFORMLY THROUGHOUT EMBRYOS OF
CC STAGES 4 AND 10. IN STAGE 16 EMBRYOS, THE EXPRESSION BECOMES
CC RESTRICTED TO THE CENTRAL NERVOUS SYSTEM, THE DEVELOPING GONADS,
CC AND A PORTION OF THE GUT. IN STAGE 17 EMBRYOS, EXPRESSION IS
CC MAINLY LOCALIZED IN CELLS ALONG THE MIDLINE OF THE CENTRAL NERVOUS
CC SYSTEM.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; AF001464; AAB58237.1; -;
DR EMBL; AE003461; AAF47027.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.016; -;
DR FlyBase; FBgn0010501; Dcp-1.
DR GO; GO:0004207; Effector caspase activity; NAS.
DR GO; GO:0030036; P-actin cytoskeleton organization and biogenesis; IMP.
DR GO; GO:0008632; P-apoptotic program; IDA.
DR GO; GO:0006922; P-cleavage of lamin; IMP.
DR GO; GO:0009795; P-embryonic morphogenesis; IMP.
DR GO; GO:0007300; P-nurse cell/oocyte transport; IMP.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1RCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 33 PROBABLE.
FT CHAIN 34 202 CASPASE-1 SUBUNIT P22.
FT PROPEP 203 215
FT CHAIN 216 323 CASPASE-1 SUBUNIT P13.
FT ACT_SITE 154 154 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 323 AA; 3126 MW; B5FF0FF75EB8E2BD CRC64;
Query Match 2.6%; Score 11; DB 1; Length 323;
Best Local Similarity 100.0%; Pred No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 277 GRPKLFFIQAC 287
Db 186 GRPKLFFIQAC 196
|||||
|||
RESULT 4
ICE DROME
ID ICE DROME STANDARD; PRT; 339 AA.
AC 001382; Q9VAH1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caspase precursor (EC 3.4.22.-) (drice).
GN ICE OR CG7788.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97327558; PubMed=9184225;
RA Fraser A.G., Evan G.I.;
RT "Identification of a Drosophila melanogaster ICE/CED-3-related
RT protease, drice.";
RL EMBO J. 16:2805-2813(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,


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MEDLINE=22380257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieff F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rub G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [6]
RN

PROCESSING:
RP MEDLINE=96353838; PubMed=8755496;
RP Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RA "In vitro activation of CPP32 and Mch3 b; h4, a novel human
RT apoptotic cysteine protease containing two ADG-like domains."
RT Proc. Natl. Acad. Sci. U.S.A. 93:7464-7467 (1996).
RL
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (REBPS). PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE 1 (AP1) AT A 216-ASP-|GLY-217
CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.
CC -!- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing. Named isoforms=3;
CC Name=Alpha;
CC IsoId=P55210-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P55210-2; Sequence=VSP 000807;
CC Note=Not proteolytically active;
CC Name=Alpha';
CC IsoId=P55210-3; Sequence=VSP 000806;
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,
CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANTZME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -!- CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4 AS BETA,
CC BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED IT ALPHA'.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL: U39613; AAC50346.1; -
CC DR
CC EMBL: U40281; AAC50352.1; -
CC DR
CC EMBL: U37448; AAC50303.1; -
CC DR
CC EMBL: U37449; AAC50304.1; -
CC DR
CC EMBL: U67319; AAC51152.1; -
CC DR
CC EMBL: U67320; AAC51153.1; -
CC DR

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OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Syrian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=8643593;
RA Pai J.-T., Brown M.S., Goldstein J.L.;
RT *Purification and cDNA cloning of a second apoptosis-related cysteine
RT protease that cleaves and activates sterol regulatory element binding
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217
CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
CC SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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CC -----
DR EMBL; U47332; AAC52595.1; -
DR HSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23 CASPASE-7 SUBUNIT P20.
FT CHAIN 24 198 BY SIMILARITY.
FT PROPEP 199 206 CASPASE-7 SUBUNIT P11.
FT CHAIN 207 303 BY SIMILARITY.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D0984648 CRC64;

Query Match 2.4%; Score 10; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186
|||||
|||||

RESULT 7
ICE7 MOUSE STANDARD; PRT; 303 AA.
ID ICE7 MOUSE
AC P97864; O08669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic

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DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McBiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT Wortmannin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid."
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molenans F., Schotte P., van Grieking W., Beyaert R.,
RA Piers W.;
RT Characterization of seven murine caspase family members."
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myer R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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 CC -----

DR EMBL; U67321; AAC53068.1; ALT_INIT.
 DR EMBL; D86353; BAA19730.1; -
 DR EMBL; Y13088; CAA73330.1; -
 DR EMBL; BC005428; AAH05428.1; -
 DR HSSP; P42574; IPAU.
 DR MEROPS; C14.304; -
 DR MGD; MGI:109383; Casp7.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR0376; ILIBCNZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P1C; 1.
 DR PROSITE; PS0208; CASPASE_P2C; 1.
 DR Hydrolase; Thiol protease; Zymoger; Apoptosis.
 KM PROPEP 1 23 BY SIMILARITY.
 FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
 FT PROPEP 199 206 BY SIMILARITY.
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
 FT ACT SITE 144 144 BY SIMILARITY.
 FT ACT SITE 186 186 BY SIMILARITY.
 FT CONFLICT 10 11 EL -> DW (IN REF. 2).
 FT CONFLICT 45 45 A -> T (IN REF. 2).
 FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
 SO SEQUENCE 303 AA; 34060 MW; 747787B5BDESF744 CRC64;

Query Match 2.4%; Score 10; DB 1; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 KPKLFFFIQAC 287
 Db 177 KPKLFFFIQAC 186
 |||||

RESULT 8

ID ICEA_HUMAN STANDARD; PRT; 521 AA.
 AC Q92851; Q8WY08; Q99845; Q9Y2U6; Q9Y2U7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caspase-10 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 4)
 DE (Apoptotic protease Mch-4) (FAS-associated death domain protein
 DE Interleukin-1B-converting enzyme 2) (FLICE2).
 GN CASP10 OR MCH4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=T-cell;
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of Cpp32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=97197836; PubMed=9045686;

RA Vincenz C., Dixit V.M.;
 RT "Fas-associated death domain protein interleukin-1beta-converting
 RT enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in
 RT CD95- and TNF-mediated death signaling";
 RL J. Biol. Chem. 272:6578-6583 (1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS B AND C), AND VARIANT ILE-410.
 RC TISSUE=Spleen, and Thymus;
 RX MEDLINE=99214592; PubMed=10187817;
 RA Ng P.W., Porter A.G., Janicke R.U.;
 RT "Molecular cloning and characterization of two novel pro-apoptotic
 RT isoforms of caspase-10";
 RL J. Biol. Chem. 274:10301-10308 (1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RX MEDLINE=21100893; PubMed=1161814;
 RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
 RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
 RA Ikeda J.-E., Hayden M.R.;
 RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
 RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
 RT critical region at chromosome 2q33-q34: candidate genes for ALS2";
 RL Genomics 71:200-213 (2001).
 RN [5]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=97121412; PubMed=8962078;
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
 RA Alnemri E.S.;
 RT "Molecular ordering of the Fas apoptotic pathway: the Fas/APO-1
 RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
 RT Ced-3/ICE-like cysteine proteases";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
 RN [6]
 RP VARIANT ALPS2 PHE-285, AND VARIANT ILE-410.
 RX MEDLINE=99339325; PubMed=10412980;
 RA Wang J., Zheng L., Lobito A., Chan F.K., Dale J., Sneller M., Yao X.,
 RA Puck J.M., Straus S.E., Lenardo M.J.;
 RT "Inherited human caspase 10 mutations underlie defective lymphocyte
 RT and dendritic cell apoptosis in autoimmune lymphoproliferative
 RT syndrome type 11";
 RL Cell 98:47-58 (1999).
 CC -/- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND
 CC TNFR-1 RECEPTORS IN A FADD DEPENDENT MANNER. MAY PARTICIPATE IN
 CC THE GRANZYME B APOPTOTIC PATHWAYS. CLEAVES AND ACTIVATES CASPASE-
 CC 3, -4, -6, -7, -8, AND -9. HYDROLYZES THE SMALL- MOLECULE
 CC SUBSTRATES, TYR-VAL-ALA-ASP-|-AMC AND ASP-GLU-VAL-ASP-|-AMC.
 CC -/- FUNCTION: ISOFORM C IS PROTEOLYTICALLY INACTIVE.
 CC -/- SUBUNIT: HETERODIMER OF A 23/17 kDa (P23/17) DEPENDENT ON THE
 CC SPLICING EVENTS AND A 12 kDa (P12) SUBUNIT.
 CC -/- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=A; Synonyms=10-A;
 CC IsoId=Q92851-1; Sequences=Displayed;
 CC Name=B; Synonyms=10-B;
 CC IsoId=Q92851-2; Sequence=VSP_000819, VSP_000820;
 CC Name=C; Synonyms=10-C;
 CC IsoId=Q92851-3; Sequence=VSP_000821, VSP_000822;
 CC -/- TISSUE SPECIFICITY: DETECTABLE IN MOST TISSUES. LOWEST EXPRESSION
 CC IS SEEN IN BRAIN, KIDNEY, PROSTATE, TESTIS, AND COLON.
 CC -/- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE
 CC THE TWO ACTIVE SUBUNITS.
 CC -/- DISEASE: Defects in CASP10 are the cause of type II autoimmune
 CC lymphoproliferative syndrome (ALPS2) [MIM:60309]. ALPS2 is
 CC characterized by abnormal lymphocyte and dendritic cell
 CC homeostasis and immune regulatory defects.
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -/- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
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CC Name=2; Synonyms=FLIP-S, CASH beta;
 CC IsoId=035732-2; Sequence=VSP_000842, VSP_000843;
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart.
 CC -!- DEVELOPMENTAL STAGE: AT EMBRYONIC DAYS E9.5 AND E10.5 HIGHEST
 CC EXPRESSION IN DEVELOPING HEART.
 CC -!- INDUCTION: ISOFORM 1 BUT NOT ISOFORM 2 IS ACTIVATED BY BCR CROSS-
 CC LINKING IN PRIMARY B-CELLS.
 CC -!- DOMAIN: THE CASPASE DOMAIN LACKS THE CTIVE SITES RESIDUES
 CC INVOLVED IN CATALYSIS
 CC -!- PTM: PROTEOLYTICALLY PROCESSED; PROBABLY BY CASPASE-8. PROCESSING
 CC LIKELY OCCURS AT THE DISC, GENERATES SUBUNIT P43 AND P12 (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
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 CC -----
 CC EMBL: Y14041; CAA74368.1; -
 CC EMBL: Y14042; CAA74369.1; -
 CC EMBL: U97076; AAC53281.1; -
 CC HSP: O15806; JODU.
 CC MEROPS: C14.974; -
 CC MGD: MG1.1336166; Cflar.
 CC InterPro: IPR001875; DED.
 CC InterPro: IPR002398; ICE.
 CC InterPro: IPR001309; ICE_p20.
 CC Pfam: PF01335; DED; 2.
 CC Pfam: PF00656; Peptidase_C14; 1.
 CC SMART: SM00115; CASC; 1.
 CC SMART: SM00031; DED; 2.
 CC PROSITE: PS0208; CASPASE_P20; 1.
 CC PROSITE: PS0168; DED; 2.
 CC Apoptosis; Repeat; Alternative splicing.
 CC CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
 CC SUBUNIT P43 (BY SIMILARITY).
 CC CASP8 AND FADD-LIKE APOPTOSIS REGULATOR
 CC SUBUNIT P12 (BY SIMILARITY).
 CC DED 1.
 CC DED 2.
 CC CASPASE.
 CC POLY-SER.
 CC LQNGRSKEPRF -> VSLEPVYGVPA (in isoform
 CC 2).
 CC /FTid=VSP_000842.
 CC Missing (in isoform 2).
 CC /FTid=VSP_000843.
 CC MISSING (IN REF. 2).
 CC CONFLICT 123 125 MISSING (IN REF. 2).
 CC SEQUENCE 484 AA; 55245 MW; 08F7A92CB09F5F:FCRC64;
 CC 2.2k; Score 9; DB 1; Length 484;
 CC Best Local Similarity 100.0%; Pred.No. 0.57;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 277 GKPKLFFIQ 285
 CC |||||
 CC Db 355 GKPKLFFIQ 363
 CC
 CC RESULT 10
 CC 9R11 ARATH
 CC ID BR11 ARATH STANDARD; PRT; 1196 AA.
 CC AC O22476;
 CC DT 15-SEP-2003 (Rel. 42, Created)
 CC DT 15-SEP-2003 (Rel. 42, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE BRASSINOSTEROID INSENSITIVE 1 precursor (EC 2.7.1.37) (AtBR11)
 CC (Brassinosteroid LRR receptor kinase).

GN BR11 OR AT4G39400 OR F23K16.30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND MUTANTS BR11-101;
 RP BR11-104; BR11-113 AND BR11-115.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=97442355; PubMed=9298904;
 RA Li J., Chory J.;
 RT "A putative leucine-rich repeat receptor kinase involved in
 RT brassinosteroid signal transduction.";
 RL Cell 90:929-938(1997).
 RN [2]
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTANTS BR11-5/DWF2-W41;
 RP BR11-6/BR11-119/DWF2-399; BR11-7/DWF2-WM3-2; BR11-8/DWF2-WM6-2 AND
 RP BR11-9/DWF2-WMB19.
 RC STRAIN=cv. Wassilewskija-2, and cv. En-2;
 RX MEDLINE=20027415; PubMed=10557222;
 RA Noguchi T., Fujioka S., Choe S., Takatsuto S., Yoshida S., Yuan H.,
 RA Feldmann K.A., Tax F.E.;
 RT "Brassinosteroid-insensitive dwarf mutants of Arabidopsis accumulate
 RT brassinosteroids.";
 RL Plant Physiol. 121:743-752(1999).
 RN [3]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, AND MUTANTS BR11-1; BR11-108; BR11-117 AND BR11-102.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20398322; PubMed=10938344;
 RA Friedrichsen D.M., Joazeiro C.A.P., Li J., Hunter T., Chory J.;
 RT "BRASSINOSTEROID-INSENSITIVE-1 is a ubiquitously expressed leucine-
 RT rich repeat receptor serine/threonine kinase.";
 RL Plant Physiol. 123:1247-1256(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083498; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Voelckert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansgor M., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermayer B., Mache R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hebeisel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weijens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenegger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W.,
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berniser S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
 RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharie M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Grandtath K., Dauner D., Herzl A.,
 RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Feilber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedror F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Iacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielle C.,
 RA Zaccaria P., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Frishman D., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Sekher A., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Maria M., Martienssen R., McCombie M.R.,
FT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana";
RL Nature 402:769-777(1999).
RN [5]
RN PHOSPHORYLATION.
RX MEDLINE=20484044; PubMed=11027724;
RA Oh M.-H., Ray W.K., Huber S.C., Asara J.M., Gage D.A., Clouse S.D.;
RT "Recombinant BRASSINOSTEROID INSENSITIVE 1 receptor-like kinase
RT autophosphorylates on serine and threonine residues and
RT phosphorylates a conserved peptide motif in vitro";
RL Plant Physiol. 124:751-766(2000).
RN [6]
RN STEROID BINDING.
RX MEDLINE=20336852; PubMed=10875920;
RA He Z., Wang Z.-Y., Li J., Zhu Q., Lamb C., Ronald P., Chory J.;
RT "Perception of brassinosteroids by the extracellular domain of the
RT receptor kinase BRI1";
RL Science 288:2360-2363(2000).
RN [7]
RN SUBCELLULAR LOCATION, STEROID BINDING, AN: JTOPHOSPHORYLATION.
RX MEDLINE=21168182; PubMed=11268216;
RA Wang Z.-Y., Seto H., Fujitaka S., Yoshida Chory J.;
RT "BRI1 is a critical component of a plasma membrane receptor for plant
RT steroids";
RL Nature 410:380-383(2001).
RN [8]
RN SUBCELLULAR LOCATION, PHOSPHORYLATION, AND INTERACTION WITH BAK1.
RX MEDLINE=22145926; PubMed=12150928;
RA Nam K.H., Li J.;
RT "BRI1/BAK1, a receptor kinase pair mediating brassinosteroid
RT signaling";
RL Cell 110:203-212(2002).
RN [9]
RN PHOSPHORYLATION, AND INTERACTION WITH BAK1.
RX MEDLINE=22145927; PubMed=12150929;
RA Li J., Wen J., Lease K.A., Duke J.T., Tax F.E., Walker J.C.;
RT "BAK1, an Arabidopsis LRR receptor-like protein kinase, interacts with
RT BRI1 and modulates brassinosteroid signaling";
RL Cell 110:213-222(2002).
CC -1- FUNCTION: Receptor with a serine/threonine-protein kinase
CC activity. Regulates, in response to brassinosteroid binding, a
CC signaling cascade involved in plant development, including
CC expression of light- and stress-regulated genes, promotion of cell
CC elongation, normal leaf and chloroplast senescence, and flowering.
CC Binds brassinolide, and less effectively castasterone, but not
CC 2,3,22,23-O-tetramethylbrassinolide or ecdysone. May be involved
CC in a feedback regulation of brassinosteroid biosynthesis.
CC Phosphorylates BRI1-associated receptor kinase 1 (BAK1).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: Activated by Ser and Thr phosphorylation.
CC -1- SUBUNIT: Heterodimer with BAK1.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
CC -1- TISSUE SPECIFICITY: Expressed ubiquitously.
CC -1- DEVELOPMENTAL STAGE: Expressed constitutively in either dark- or
CC light-grown seedlings.
CC -1- DOMAIN: Contains one leucine-zipper motif and two pairs of
CC conservatively spaced Cys (Cys pair 1 and 2) involved in forming
CC heterodimers.
CC -1- PTM: Phosphorylated on at least 12 sites, with a preference for
CC Ser residues.
CC -1- MISCELLANEOUS: A 70 amino acid island between the 20th and the
CC 21th LRR is essential for the binding of brassinosteroids.
CC -1- MISCELLANEOUS: Binding of brassinosteroid induces intramolecular
CC autophosphorylation of BRI1. Interaction with BAK1 activates both

CC receptor kinases and the full activation of either receptor kinase
CC requires transphosphorylation by their partners. Optimum in vitro
CC phosphorylation of the substrate requires Arg or Lys residues at
CC P-3, P-4, and P-5 (relative to the phosphorylated amino acid at
CC P=0).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: Contains 25 leucine-rich (LRR) repeats.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF017056; AAC49810.1; -
CC EMBL; AL078620; CAB44675.1; -
CC EMBL; AL161595; CAB80603.1; -
CC PIR; T09356; T09356.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR007090; LRR_plant.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00560; LRR; 17.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Kinase; Serine/threonine-protein kinase; Receptor;
CC Steroid-binding; ATP-binding; Repeat; Signal; Transmembrane;
CC Leucine-rich repeat; Glycoprotein; Phosphorylation.
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 1196 BRASSINOSTEROID INSENSITIVE 1.
CC TRANSMEM 793 813 POTENTIAL.
CC REPEAT 98 121 LRR 1.
CC REPEAT 122 146 LRR 2.
CC REPEAT 148 169 LRR 3.
CC REPEAT 172 197 LRR 4.
CC REPEAT 199 221 LRR 5.
CC REPEAT 222 244 LRR 6.
CC REPEAT 245 268 LRR 7.
CC REPEAT 269 290 LRR 8.
CC Query Match 2.2%; Score 9; DB 1; Length 1196;
CC Best Local Similarity 100.0%; Pred.No.1.3;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC QY 131 IGSGGFGDV 139
CC DB 889 IGSGGFGDV 897
CC |||||
CC RESULT 11
CC YK10_ARCFU
CC ID YK10_ARCFU STANDARD; PRT; 232 AA.
CC AC 028269;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Hypothetical protein AF2010.
CC GN AF2010.
CC OS Archaeoglobus fulgidus.
CC OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
CC OC Archaeoglobaceae; Archaeoglobus.
CC OX NCBI_TaxID=2234;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- MISCELLANEOUS: A 68 amino acid island between the 20th and the
 CC 21th LRR is essential for the binding of brassinosteroids (By
 CC similarity).
 CC -!- MISCELLANEOUS: Bril1 is almost identical to SR160, a systemin
 CC receptor identified in *Lycopersicon peruvianum*. Competition
 CC experiments indicate that brassinosteroid and systemin are
 CC probably perceived by different regions of the receptor.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: Contains 24 leucine-rich (LRR) repeats.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AV179606; AAN85409.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR007090; LRR_plant.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00560; LRR; 18.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00019; LEURICHRPT.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR Plant defense; Transferase; Kinase; Serine/threonine-protein kinase;
 KW Receptor; ATP-binding; Steroid-binding; Repeat; Signal; Transmembrane;
 KW Leucine-rich repeat; Glycoprotein.
 FT SIGNAL 1 34 POTENTIAL
 FT CHAIN 35 1207 BRASSINOSTEROID LRR RECEPTOR KINASE.
 FT TRANSMEM 803 823 POTENTIAL.
 FT REPEAT 80 106 LRR 1.
 FT REPEAT 107 131 LRR 2.
 FT REPEAT 133 158 LRR 3.
 FT REPEAT 159 182 LRR 4.
 FT REPEAT 184 206 LRR 5.
 FT REPEAT 211 235 LRR 6.
 FT REPEAT 237 255 LRR 7.
 FT REPEAT 256 280 LRR 8.
 FT REPEAT 282 307 LRR 9.
 FT REPEAT 327 350 LRR 10.
 FT REPEAT 351 375 LRR 11.
 FT REPEAT 376 399 LRR 12.
 FT REPEAT 400 424 LRR 13.
 FT REPEAT 426 450 LRR 14.
 FT REPEAT 452 474 LRR 15.
 FT REPEAT 475 498 LRR 16.
 FT REPEAT 499 522 LRR 17.
 FT REPEAT 524 546 LRR 18.
 FT REPEAT 547 570 LRR 19.
 FT REPEAT 572 594 LRR 20.
 FT REPEAT 662 686 LRR 21.
 FT REPEAT 687 709 LRR 22.
 FT REPEAT 710 734 LRR 23.
 FT REPEAT 735 759 LRR 24.
 FT DOMAIN 888 1163 PROTEIN KINASE.
 FT NP_BIND 894 902 ATP (BY SIMILARITY).
 FT BINDING 916 916 ATP (BY SIMILARITY).
 FT ACT_SITE 1014 1014 BY SIMILARITY.
 FT SITE 71 78 CYS PAIR 1.
 FT SITE 771 779 CYS PAIR 2.
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 556 556 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 662 662 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 746 746 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MUTAGEN 1012 1012 H->Y: IN CUS-ABS; BRASSINOSTEROID-
 FT INSENSITIVE SEMI-DWARF MUTANT.
 SQ SEQUENCE 1207 AA; 131956 MW; 6C370BA048060B7F CRC64;
 Query Match 1.9%; Score 8; DB 1; Length 1207;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 132 GSGGFGDV 139
 DB 895 GSGGFGDV 902
 ID BR11_LYCPE STANDARD; PRT; 1207 AA.
 AC Q8L899;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Systemin receptor SR160 precursor (EC 2.7.1.37) (Brassinosteroid LRR
 DE receptor kinase).
 OS *Lycopersicon peruvianum* (Peruvian tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4082;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 101-311; 432-440; 548-554 AND 862-874,
 RP GLYCOSYLATION, AND SUBSTRATE BINDING.
 RX MEDLINE=22103620; PubMed=12060717;
 RA Scheer J.M., Ryan C.A. Jr.;
 RT "The systemin receptor SR160 from *Lycopersicon peruvianum* is a member
 RT of the LRR receptor kinase family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9585-9590(2002).
 CC -!- FUNCTION: Receptor with a serine/threonine-protein kinase
 CC activity. Involved in the perception of systemin, a peptide
 CC hormone responsible for the systemic activation of defense genes
 CC in leaves of wounded plants. May also regulate, in response to
 CC brassinosteroid binding, a signaling cascade involved in plant
 CC development (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- PTM: Glycosylated.
 CC -!- MISCELLANEOUS: A 68 amino acid island between the 20th and the
 CC 21th LRR is essential for the binding of brassinosteroids (By
 CC similarity).
 CC -!- MISCELLANEOUS: SR160 is almost identical to Bril1, a
 CC brassinosteroid receptor identified in *Lycopersicon esculentum*.
 CC Competition experiments indicate that brassinosteroid and systemin
 CC are probably perceived by different regions of the receptor.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: Contains 24 leucine-rich (LRR) repeats.
 CC -----
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EMBL; AY112661; AAM48285.1; -
InterPro; IPR001611; LRR.
InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_kinase.
Pfam; PF00560; LRR; 19.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00019; LEURICHRPT.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TK; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Plant defense; Transferase; Kinase; Serine/threonine-protein kinase;
Receptor; ATP-binding; Steroid-binding; Repeat; Signal; Transmembrane;
Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 34
FT CHAIN 35 1207
FT TRANSMEM 803 823
FT REPEAT 80 106
FT REPEAT 107 121
FT REPEAT 133 158
FT REPEAT 159 182
FT REPEAT 184 206
FT REPEAT 211 235
FT REPEAT 237 255
FT REPEAT 256 280
FT REPEAT 282 307
FT REPEAT 327 350
FT REPEAT 351 375
FT REPEAT 376 399
FT REPEAT 400 424
FT REPEAT 426 450
FT REPEAT 452 474
FT REPEAT 475 498
FT REPEAT 499 522
FT REPEAT 524 546
FT REPEAT 547 570
FT REPEAT 572 594
FT REPEAT 662 686
FT REPEAT 687 709
FT REPEAT 710 734
FT REPEAT 735 759
FT DOMAIN 888 1163
FT NP_BIND 894 902
FT BINDING 916 916
FT ACT_SITE 1014 1014
FT SITE 71 78
FT SITE 771 779
FT CARBOHYD 119 119
FT CARBOHYD 166 166
FT CARBOHYD 196 196
FT CARBOHYD 235 235
FT CARBOHYD 245 245
FT CARBOHYD 287 287
FT CARBOHYD 339 339
FT CARBOHYD 363 363
FT CARBOHYD 412 412
FT CARBOHYD 449 449
FT CARBOHYD 521 521
FT CARBOHYD 556 556
FT CARBOHYD 584 584
FT CARBOHYD 646 646
FT CARBOHYD 662 662
FT CARBOHYD 724 724

FT CARBOHYD 746 746 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 767 767 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1207 AA; 131963 MW; 1422D1DFDA458073 CRC64;
Query Match 1.9%; Score 8; DB 1; Length 1207;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 132 GSGGFGDV 139
Db 895 GSGGFGDV 902
RESULT 15
RPOC_CHLPN STANDARD; PRT: 1393 AA.
ID AC Q92999; Q9JSJ7; O9K211;
DT 10-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
beta' chain) [RNA polymerase beta' subunit].
GN RPOC OR CPN0082 OR CP0693.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
[RNA](N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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DR EMBL: AE001593; AAD18235.1;
DR EMBL: AE002228; AAF38501.1; ALT_INIT.
DR EMBL: AP002545; BAA98292.1;
DR PIR: B86501; B86501.
DR PIR: E72122; E72122.
DR HSP: Q9KWU6; 1HQM.
DR TIGR: CP0693;
DR InterPro: IPR007022; RNA_pol_A.
DR InterPro: IPR007080; RNA_pol_Rpb1_1.
DR InterPro: IPR007066; RNA_pol_Rpb1_3.
DR InterPro: IPR007083; RNA_pol_Rpb1_4.
DR InterPro: IPR007081; RNA_pol_Rpb1_5.
DR InterPro: IPR006592; RNA_pol_A_N.
DR Pfam: PF04997; RNA_pol_Rpb1_1.
DR Pfam: PF00623; RNA_pol_Rpb1_2.
DR Pfam: PF04983; RNA_pol_Rpb1_3.
DR Pfam: PF05000; RNA_pol_Rpb1_4.
DR Pfam: PF04998; RNA_pol_Rpb1_5.
DR SMART: SM00663; RPOA_N; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription;
FT Complete proteome.
FT CONFLICT 1031 1031 A -> G (IN REF. 1).
SQ SEQUENCE 1393 AA; 154900 MW; E0734EF236C6FDE8 CRC64;

Query Match 1.9%; Score 8; DB 1; Length 1393;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SEDLQSL 384
DB 194 SEDLQSL 201
|||||

RESULT 16
GCSE MYCLE STANDARD; PRT; 132 AA.
AC Q32920;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable glycine cleavage system H protein.
GN GCVH OR M2077 OR MLCB1788.37C.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby K., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford I.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrall B.G.;
RA "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF
CC GLYCINE. THE H PROTEIN SHUTTLES THE METHYLAMINE GROUP OF GLYCINE
CC FROM THE P PROTEIN TO THE T PROTEIN (BY SIMILARITY).
CC -!- COFACTOR: THE H CHAIN CONTAINS A COVALENTLY-BOUND LIPOYL COFACTOR
CC (BY SIMILARITY).
CC -!- SUBUNIT: The glycine cleavage system is composed of four proteins:
CC P, T, L, and H (By similarity).
CC -!- SIMILARITY: Belongs to the gcvH family.
CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL008609; CAA15469.1;
DR EMBL: AL583924; CAC31032.1;
DR PIR: T44759; T44759.
DR HSP: P16048; 1HTP.
DR LepToma; ML2077;
DR HAMAP; MF_00272; 1.
DR InterPro: IPR002930; GCV_H.
DR InterPro: IPR003016; Lipoyl.
DR Pfam: PF01597; GCV_H; 1.
DR TIGRPFAM: TIGR00527; gcvH; 1.
DR PROSITE: PS00189; LIPOYL; 1.
KW Lipoyl; Complete proteome.
FT BINDING 65 65 LIPOYL (BY SIMILARITY).
SQ SEQUENCE 132 AA; 14070 MW; 2DBFC5D69BA1C6AA CRC64;

Query Match 1.7%; Score 7; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 DVGALES 144
DB 109 DVGALES 115
|||||

RESULT 17
PTH_CHLPN STANDARD; PRT; 180 AA.
AC Q9Z6V6; Q9JQC0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH).
GN PTH OR CPN0950 OR CP0909.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- FUNCTION: The natural substrate for this enzyme may be peptidyl-
CC tRNAs which drop off the ribosome during protein synthesis (By

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CC CC CATALYTIC ACTIVITY: N-substituted aminoacyl-tRNA + H(2)O = N-
CC substituted amino acid + tRNA.
CC
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the PTH family.
CC
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CC
CC EMBL; AE001675; AAD19088.1; -
CC EMBL; AE002250; AAF38694.1; -
CC EMBL; AP002548; BAA99158.1; -
CC PIR; D86609; D86609.
CC PIR; E72014; E72014.
CC HSSP; P23932; 2PTH.
CC TIGR; CP0909.
CC
CC HAWAP; MF_00083; -; 1.
CC InterPro; IPR001328; Pept tRNA hydro.
CC Pfam; PF01195; Pept tRNA hydro; 1.
CC ProDom; PD005324; Pept tRNA hydro; 1.
CC ProSITE; PS01195; PEPT_TRNA_HYDROL_1; 1.
CC ProSITE; PS01196; PEPT_TRNA_HYDROL_2; 1.
CC Hydrolase; Complete proteome.
CC
CC QUERY MATCH 1.7%; Score 7; DB 1; Length 180;
CC Best Local Similarity 100.0%; Pred. No. 26;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 15 RLVEELQ 21
CC DB 29 RLVEELQ 35
CC
CC RESULT 18
CC HN2_XENLA STANDARD; PRT; 196 AA.
CC ID HN2_XENLA
CC AC P42587;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein XENK-2.
CC OS Xenopus laevis (African clawed frog).
CC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
CC Xenopodinae; Xenopus.
CC NCBI_TaxID=8355;
CC
CC RP SEQUENCE FROM N.A.
CC TISSUE=Embryonic head;
CC MEDLINE=93387212; PubMed=8104140;
CC Saha M.S., Michel R.B., Guldinger K.M., Grainger R.M.;
CC "A Xenopus homeobox gene defines dorsal-ventral domains in the
CC developing brain.";
CC
CC RL DEVELOPMENT 118:193-202(1993).
CC
CC -!- FUNCTION: DEFINES DORSAL-VENTRAL DOMAINS IN DEVELOPING BRAIN. MAY
CC PLAY A ROLE IN DEFINING POSITIONAL INFORMATION ALONG THE
CC ANTERIOR-POSTERIOR (A/P) AXIS AND THE DORSAL-VENTRAL (D/V) AXIS OF
CC THE DEVELOPING NERVOUS SYSTEM. MAY BE INVOLVED IN DETERMINING
CC POSITIONAL OR BOUNDARY INFORMATION RATHER THAN DETERMINING A GIVEN
CC CELL TYPE.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: FOREBRAIN AND MIDBRAIN.
CC -!- DEVELOPMENTAL STAGE: IS FIRST DETECTABLE IN LATER NEURAL STAGES
CC (STAGE 14). LEVELS GRADUALLY INCREASE DURING LATER NEURAL STAGES
CC AND BECOMES FAIRLY CONSTANT THROUGHOUT TAILBUD AND HATCHING STAGES
CC BEFORE DECLINING AT LATE SWIMMING TADPOLE STAGES.

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CC CC -!- SIMILARITY: BELONGS TO THE NK-2 HOMEODOMAIN FAMILY.
CC
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CC
CC EMBL; LI0327; AAA72342.1; -
CC EMBL; S65507; AAB28271.2; -
CC HSSP; P22808; LNK3.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC ProSITE; PS00027; HOMEODOMAIN_1; 1.
CC ProSITE; PS00071; HOMEODOMAIN_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
CC DNA_BIND 69 128 HOMEODOMAIN.
CC SQ SEQUENCE 196 AA; 22809 MW; F5A0657470C1031B CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 196;
CC Best Local Similarity 100.0%; Pred. No. 28;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 110 VLRLPEIR 116
CC DB 31 VLRLPEIR 37
CC
CC RESULT 19
CC GDB_RHIL0 STANDARD; PRT; 210 AA.
CC ID GDB_RHIL0
CC AC Q98D22;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Methyltransferase gldb (EC 2.1.1.-) (Glucose inhibited division
CC protein B).
CC GN RHIZOB IRL4481.
CC OS Rhizobium loti (Mesorhizobium loti).
CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC Phyllobacteriaceae; Mesorhizobium.
CC NCBI_TaxID=381;
CC
CC RP SEQUENCE FROM N.A.
CC STRAIN=MAFF303099;
CC MEDLINE=21082930; PubMed=11214968;
CC Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
CC Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
CC Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
CC Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
CC Takeuchi C., Yamada M., Tabata S.;
CC "Complete genome structure of the nitrogen-fixing symbiotic bacterium
CC Mesorhizobium loti.";
CC DNA Res. 7:331-338(2000).
CC
CC -!- FUNCTION: Probable S-adenosyl-L-methionine dependent
CC methyltransferase specific for a sterol and/or lipid substrate (By
CC similarity).
CC
CC -!- SIMILARITY: BELONGS TO THE GDB FAMILY.
CC
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CC
CC EMBL; AP003004; BAB51128.1; -
CC HAWAP; MF_00074; -; 1.

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DR InterPro: IPR003682; GidB.
DR Pfam: PF02527; GidB: 1.
DR ProDom: PD004441; GidB: 1.
DR TIGRFAMs: TIGR00136; GidB: 1.
KW Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 210 AA; 23107 MW; F798AB0C33328AB CRC64;

Query Match 1.7%; Score 7; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 VDIGSGG 135
DB 71 VDIGSGG 7

RESULT 20
RS3_RALSO STANDARD; PRT; 264 AA.
ID RS3_RALSO
AC Q8XV18;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S3.
GN RPSC OR RSC3013 OR RS01076.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=1823852;
RA Salanoubat M., Genin S., Artiguenave F., Couzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
RL
CC -!- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
CC in the 70S ribosome, positioning it for translation (By
CC similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
CC with proteins S10 and S14 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC
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CC
CC EMBL: AL646073; CAD16722.1; -.
CC HAMAP: MF_01309; -.
CC InterPro: IPR004087; KH_dom.
CC InterPro: IPR004044; KH_TYPE_2.
CC InterPro: IPR001351; Ribosomal_S3.
CC InterPro: IPR005704; S3_bact.
CC Pfam: PF00013; KH; 1.
CC Pfam: PF00189; Ribosomal_S3_C; 1.
CC Pfam: PF00417; Ribosomal_S3_N; 1.
CC SMART: SM00322; KH; 1.
CC TIGRFAMs: TIGR01009; rpsC_bact; 1.
CC PROSITE: PS50823; KH_TYPE_2; 1.
CC PROSITE: PS00548; RIBOSOMAL_S3; 1.
CC Ribosomal protein; RNA-binding; Complete proteome.
KW DOMAIN 39 107 KH TYPE-2.
FT DOMAIN 39 107 KH TYPE-2.
SQ SEQUENCE 264 AA; 29738 MW; 72BBCACF1EC2DD03E CRC64;

Query Match 1.7%; Score 7; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 VDIGSGG 135
DB 71 VDIGSGG 7

RESULT 20
RS3_RALSO STANDARD; PRT; 264 AA.
ID RS3_RALSO
AC Q8XV18;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S3.
GN RPSC OR RSC3013 OR RS01076.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=1823852;
RA Salanoubat M., Genin S., Artiguenave F., Couzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RT Nature 415:497-502(2002).
RL
CC -!- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
CC in the 70S ribosome, positioning it for translation (By
CC similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
CC with proteins S10 and S14 (By similarity).
CC -!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC
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CC
CC EMBL: AL646073; CAD16722.1; -.
CC HAMAP: MF_01309; -.
CC InterPro: IPR004087; KH_dom.
CC InterPro: IPR004044; KH_TYPE_2.
CC InterPro: IPR001351; Ribosomal_S3.
CC InterPro: IPR005704; S3_bact.
CC Pfam: PF00013; KH; 1.
CC Pfam: PF00189; Ribosomal_S3_C; 1.
CC Pfam: PF00417; Ribosomal_S3_N; 1.
CC SMART: SM00322; KH; 1.
CC TIGRFAMs: TIGR01009; rpsC_bact; 1.
CC PROSITE: PS50823; KH_TYPE_2; 1.
CC PROSITE: PS00548; RIBOSOMAL_S3; 1.
CC Ribosomal protein; RNA-binding; Complete proteome.
KW DOMAIN 39 107 KH TYPE-2.
FT DOMAIN 39 107 KH TYPE-2.
SQ SEQUENCE 264 AA; 29738 MW; 72BBCACF1EC2DD03E CRC64;

Query Match 1.7%; Score 7; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 EIRKPEV 120
DB 105 EIRKPEV 111

RESULT 21
NHS_STRAS STANDARD; PRT; 274 AA.
ID NHS_STRAS
AC P52391;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 23S rRNA methyltransferase (EC 2.1.1.-) (23S rRNA methylase).
GN NHS.
OS Streptomyces actuosus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1885;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25421;
RX MEDLINE=90382703; PubMed=2401410;
RA Li Y., Dosch D.C., Strohl W.R., Floss H.G.;
RA "Nucleotide sequence and transcriptional analysis of the nosiheptide-
RT resistance gene from Streptomyces actuosus.";
RL Gene 91:9-17(1990).
CC -!- FUNCTION: CONFERS RESISTANCE TO ANTIBIOTIC NOSIHEPTIDE.
CC -!- SIMILARITY: TO S-AZUREUS TSR.
CC
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CC
CC EMBL: U75434; AAB17875.1; -.
CC PIR: JQ0686; JQ0686.
CC InterPro: IPR001537; SpoU_methylase.
CC InterPro: IPR006795; TSNR_N.
CC Pfam: PF00588; SpoU_methylase; 1.
CC Pfam: PF04705; TSNR_N; 1.
CC ProDom: PD001243; SpoU_methylase; 1.
CC Antibiotic resistance; Transferase; Methyltransferase.
KW Antibioc resistance; Transferase; Methyltransferase.
SQ SEQUENCE 274 AA; 29183 MW; 9FA2C12B2E8BF24D CRC64;

Query Match 1.7%; Score 7; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADRRLLR 10
DB 156 ADRRLLR 162

RESULT 22
SDSB_PSES9 STANDARD; PRT; 306 AA.
ID SDSB_PSES9
AC P52686;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE SDS degradation transcriptional activation protein.
GN SDSB.
OS Pseudomonas sp. (strain ATCC 19151).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=315;
```

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RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92267380; PubMed=1587481;
RA  Davison J., Brunel P., Phanopoulos A., Prozzi D., Terpstra P.;
RT  "Cloning and sequencing of pseudomonas genes determining sodium
RL  dodecyl sulfate biodegradation.";
RL  Gene 114:19-24(1992).
CC  -!- FUNCTION: ACTIVATES THE TRANSCRIPTION OF THE SDS GENE FOR
CC  SODIUM DODECYL SULFATE (SDS) DEGRADATION.
CC  -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC  REGULATORS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M86744; AAA25988.1; -
CC  InterPro; IPR000947; HTH_LySR.
CC  InterPro; IPR005119; LySR_subst.
CC  Pfam; PF00126; HTH_1; 1.
CC  Pfam; PF03466; LySR_substrate; 1.
CC  PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
CC  Transcription regulation; DNA-binding; Activator.
CC  DNA_BIND 19 38 H-T-H MOTIF (POTENTIAL).
CC  SEQUENCE 306 AA; 32955 MW; BE1A6EACF3FE24FA CRC64;
CC  -----
CC  Query Match 1.7%; Score 7; DB 1; Length 306;
CC  Best Local Similarity 100.0%; Pred. No. 42;
CC  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC  -----
Qy 214 LALLELA 220
Db 256 LALLELA 262
| | | | |
| | | | |

RESULT 23
G3P_THEVO STANDARD; PRT; 338 #
AC G97BJ8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (E: 1.2.1.59) (GAPDH)
GN GAP OR TW0457 OR TVG0444310.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GSSI / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Anano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima O.Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RL sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-1426 (2000).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(P)(+) = 3-phospho-D-glyceroyl phosphate + NAD(P)H.
CC -!- PATHWAY: Second phase of glycolysis; first step.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF000992; BAB59599.1; -
CC HAMAP; MF_00559; -; 1.
CC InterPro; IPR000173; GAP_dhdrogenase.
CC InterPro; IPR006436; GAPDH-II_archae.
CC Pfam; PF00044; gpdh; 1.
CC Pfam; PF02800; gpdh_C; 1.
CC ProDom; PD007761; GAPDH-II_archae; 1.
CC TIGRFAMs; TIGR01546; GAPDH-II_archae; 1.
CC PROSITE; PS00071; GAPDH; 1.
CC Glycolysis; Oxidoreductase; NAD; NADP; Complete proteome.
KW BINDING 139 139 GLYCERALDEHYDE 3-PHOSPHATE (BY
FT SIMILARITY).
FT SEQUENCE 338 AA; 37374 MW; C9BD53DFD4722F34 CRC64;
CC -----
CC Query Match 1.7%; Score 7; DB 1; Length 338;
CC Best Local Similarity 100.0%; Pred. No. 46;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
Qy 386 RVANAVS 392
Db 15 RVANAVS 21
| | | | |
| | | | |

RESULT 24
TRPD_AERPE STANDARD; PRT; 345 AA.
ID TRPD_AERPE
AC G9Y8T2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anthranilate phosphoribosyltransferase (EC 2.4.2.18).
GN TRPD OR APE2551.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K1;
RX MEDLINE=9910339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kobugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RL crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosylpyrophosphate =
CC N-5'-phosphoribosyl-anthranilate + diphosphate.
CC -!- PATHWAY: tryptophan biosynthesis; second step.
CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE
CC FAMILY.
CC -----
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CC -----
CC EMBL; AF000064; BAA81568.1; -
CC PIR; H72488; H72488.
CC HAMAP; MF_00211; -; 1.
CC InterPro; IPR005940; Ant_phospho_trans.

```


RX MEDLINE=93339575; PubMed=8393417;
 RA Glazebrook J., Ichige A., Walker G.C.;
 RT "A Rhizobium meliloti homolog of the Escherichia coli peptide-
 RT antibiotic transport protein SbmA is essential for bacteroid
 RL development."; Genes Dev. 7:1485-1497(1993).
 RN [2].
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puhler A.;
 RT "The complete sequence of the 1,583-kb pSymB megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 RL CC -!- FUNCTION: FUNCTIONS IN THE TRANSPORT OF MOLECULES, POSSIBLY
 CC PEPTIDES, ACROSS THE INNER MEMBRANE. IS ESSENTIAL FOR BACTEROID
 CC DEVELOPMENT.
 CC ! SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -!- TISSUE SPECIFICITY: NODULI.
 CC -!- SIMILARITY: STRONG, TO E. COLI SBMA.
 CC
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 CC
 DR EMBL; X73522; CAA51918.1; -;
 DR EMBL; AL603646; CAC49525.1; -;
 DR PIR; A47649; A47649.
 DR PIR; E95982; E95982.
 KW Transmembrane; Inner membrane; Plasmid; Complete proteome.
 FT TRANSMEM 1; 31 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 143 163 POTENTIAL.
 FT TRANSMEM 210 230 POTENTIAL.
 FT TRANSMEM 247 267 POTENTIAL.
 FT TRANSMEM 336 356 POTENTIAL.
 FT CONFLICT 128 128 A -> P (IN REF. 1).
 SQ SEQUENCE 420 AA; 47848 MW; 548496A86AD 30FE CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 420;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 278 KPKLFFI 284
 DB 8 KPKLFFI 14
 RESULT 28
 IFR2_HUMAN
 ID IFR2_HUMAN STANDARD; PRT; 442 AA.
 AC Q12894;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Interferon-related developmental regulator 2 (SKMCL5 protein).
 GN IFRD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danté M., Wamsley P.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, Muscle, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3].
 RN RP SEQUENCE OF 2-442 FROM N.A.
 RC TISSUE=Skeletal muscle
 RX MEDLINE=97203201; PubMed=9050919;
 RA Latif F., Duh F.-M., Bader S., Sekido Y., Li H., Geil L., Zbar B.,
 RA Minna J.D., Lerman M.I.;
 RT "The human homolog of the rodent immediate early response genes, PC4
 RT and TIS7, resides in the lung cancer tumor suppressor gene region on
 RT chromosome 3p21."; Hum. Genet. 99:334-341(1997).
 RL CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -!- SIMILARITY: BELONGS TO THE IFRD FAMILY.
 CC
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 CC
 DR EMBL; U73167; AAC02728.1; -;
 DR EMBL; BC001676; AAH01676.1; -;
 DR EMBL; BC007265; AAH07265.1; -;
 DR EMBL; BC007437; AAH07437.1; -;
 DR EMBL; U09585; AAC16924.1; -;
 DR Genew; HGNC:5457; IFRD2.
 DR MIM; 602725;
 DR GO; GO:0030154; P:cell differentiation; ISS.
 DR GO; GO:0008283; P:cell proliferation; ISS.
 DR InterPro; IPR006921; IFRD_C.
 DR Pfam; PF05004; IFRD; 1.
 DR Pfam; PF04836; IFRD_C; 1.
 SQ SEQUENCE 442 AA; 48047 MW; CB54F2118C0CBA74 CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 442;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 140 GALESRL 146
 DB 94 GALESRL 100
 RESULT 29
 ICE8_MOUSE
 ID ICE8_MOUSE STANDARD; PRT; 480 AA.
 AC O89110; O35669;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)
Caspase-8 precursor (EC 3.4.22.-).
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129/SvJ;
RX MEDLINE=98316661; PubMed=9654089;
RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8.";
RL Eur. J. Biochem. 253:399-405(1998).
[2]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99057979; PubMed=9837723;
RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
RA van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
RA Vandenaabeele P.;
RT "Molecular cloning and identification of murine caspase-8.";
RL J. Mol. Biol. 284:1017-1026(1998).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zdobych B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., McKusick R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN SEQUENCE OF 57-476 FROM N.A.
RA Kioschis P., Kischkel F., Poustka A., Kramer P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M8 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Likely target for the coxsack virus CRMA death inhibitory protein.
CC -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
CC Interacts with FADD and CFLAR (by similarity).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
CC Highest expression in spleen, thymus, lung, liver and kidney.
CC Lower expression in heart, brain, testis and skeletal muscle.
CC -!- DEVELOPMENTAL STAGE: In the embryo, high expression occurs at
CC day 7.
CC -!- PTM: Generation of the subunits requires association with the
CC death-inducing signaling complex (DISC), whereas additional
CC processing is likely due to the autocatalytic activity of the

activated protease. G2M8 and CASP10 can be involved in these
processing events (by similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
-!- SIMILARITY: Contains 2 death effector (DED) domains.
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EMBL; AF067841; AAC40132.1; JOINED.
EMBL; AF067835; AAC40132.1; JOINED.
EMBL; AF067836; AAC40132.1; JOINED.
EMBL; AF067837; AAC40132.1; JOINED.
EMBL; AF067838; AAC40132.1; JOINED.
EMBL; AF067839; AAC40132.1; JOINED.
EMBL; AF067840; AAC40132.1; JOINED.
EMBL; AF067834; AAC40131.1; -
EMBL; AJ007749; CAA07677.1; -
EMBL; BC006737; AAH06737.1; -
EMBL; AJ000641; CAA04196.1; -
HSSP; Q15806; IQDUP.
MEROPS; C14.009; -
MGD; MGI:1261423; Casp8.
GO; GO:0005737; Cytoplasm; IDA.
GO; GO:0005634; Nucleus; IDA.
GO; GO:004205; P: caspase-8 activity; IDA.
GO; GO:0006915; P: apoptosis; IDA.
InterPro; IPR001875; DED.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF01335; DED; 2.
Pfam; PF00656; Peptidase C14; 1.
PRINTS; PR00376; IL18CENZYME.
SMART; SM00115; CASC; 1.
SMART; SM00031; DED; 2.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
PROSITE; PS0168; DED; 2.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Repeat.
FT PROPEP 1 218
FT CHAIN 219 376
FT CASPASE-8 SUBUNIT P18.
FT PROPEP 377 387
FT BY SIMILARITY.
FT CHAIN 388 480
FT CASPASE-8 SUBUNIT P10.
FT ACT_SITE 319 319
FT BY SIMILARITY.
FT ACT_SITE 362 362
FT BY SIMILARITY.
FT DOMAIN 3 80
FT DED 1.
FT DOMAIN 101 177
FT DED 2.
FT CONFLICT 68 71
FT HISR -> PHVGV (IN REF. 4).
FT CONFLICT 94 99
FT DNAQIS -> ROCPRFL (IN REF. 4).
FT CONFLICT 96 96
FT A -> V (IN REF. 2).
FT CONFLICT 103 107
FT VMLFK -> SCSFR (IN REF. 4).
FT CONFLICT K -> N (IN REF. 4).
SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5D4F CRC64;
Query Match 1.74; Score 7; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 407 LRKKLFF 413
Db 472 LRKKLFF 478
RESULT 30
PHOQ_SALTY STANDARD; PRT; 487 AA.
ID PHOQ_SALTY

AC DT 01-JAN-1990 (Rel. 13, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Virulence sensor protein phoQ (EC 2.7.3.-)
GN PHOQ OR STM1230.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=ATCC 14028;
RX MEDLINE=89296942; PubMed=2544889;
RA Miller S.I., Kukral A.M., Mekalanos J.J.;
RT "A two-component regulatory system (phoP phoQ) controls Salmonella
RT typhimurium virulence.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5054-5058 (1989).
RN [2]
RN SEQUENCE FROM N.A. AND MUTAGENESIS OF ARG-31.
RP STRAIN=SL1344;
RX MEDLINE=21437654; PubMed=11553591;
RA Cano D.A., Martinez-Moya M., Pucciarelli M.G., Groisman E.A.,
RA Cabadeus J., Garcia-del Portillo F.;
RT "Salmonella enterica serovar Typhimurium response involved in
RT attenuation of pathogen intracellular proliferation.";
RL Infect. Immun. 69:6463-6474 (2001).
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Tifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856 (2001).
CC -!- FUNCTION: Member of the two-component regulatory system phoQ/phoP
CC which regulates the expression of genes involved in virulence and
CC promotes intramacrophage survival of S.typhimurium. Is required to
CC attenuate bacterial growth within fibroblast cells. PhoQ may
CC function as a membrane-associated protein kinase that
CC phosphorylates phoP in response to environmental signals.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- SIMILARITY: Contains 1 HAMP domain.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.

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CC EMBL; M24424; AAA27189.1; -
CC EMBL; AJ272210; CAB75592.1; -
CC EMBL; AE008753; AAL20159.1; -
CC STyGene; SG10294; phoQ.
CC InterPro; IPR003594; ATPbind ATPase.
CC InterPro; IPR004358; Bact_sens_pr_C.
CC InterPro; IPR003660; HAMP.
CC InterPro; IPR003661; His_kinA.
CC InterPro; IPR005467; His_kinase.
CC Pfam; PF00672; HAMP; 1.
CC Pfam; PF02518; HATPase_C; 1.
CC Pfam; PF00512; HisKA; 1.
CC PRINTS; PM00344; BCTRLSENSOR.
CC SMART; SM00387; HATPase_C; 1.
CC SMART; SM00388; HisKA; 1.

DR PROSITE; PSS0885; HAMP; 1.
DR PROSITE; PSS0109; HIS_KIN; 1.
KW Sensory transduction; Transferase; Kinase; Phosphorylation;
KW Transmembrane; Inner membrane; Growth regulation; Virulence;
KW Complete proteome.
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 17 37 POTENTIAL.
FT DOMAIN 38 194 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 195 215 POTENTIAL.
FT DOMAIN 216 487 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 216 266 HAMP.
FT DOMAIN 274 481 HISTIDINE KINASE.
FT MOD_RES 277 277 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARIANT 82 99 MISSING (IN STRAIN ATCC 10428).
FT VARIANT 442 459 MISSING (IN STRAIN ATCC 10428).
FT MUTAGEN 313 313 R->W: INCREASED ABILITY TO PROLIFERATE
FT WITHIN FIBROBLASTS.
SQ SEQUENCE 487 AA; 55466 MW; BDCFEFC56F4CA058 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 VLLSREL 34
Db 332 VLLSREL 338
|||||

RESULT 31
PSS5_HUMAN
ID PSS5_HUMAN STANDARD; PRT; 504 AA.
AC Q16401; Q15045;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 26S proteasome non-ATPase regulatory subunit 5 (26S proteasome
DE subunit S5B) (26S proteasome subunit S5 basic).
GN PSMD5 OR KIAA0072.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 75:96; 311-337 AND 431-449.
RC TISSUE=Breast cancer.
RX MEDLINE=96007524; PubMed=7559544;
RA Devereaux Q., Jensen C., Rechsteiner M.;
RT "Molecular cloning and expression of a 26 S protease subunit enriched
RL in diluicene repeats.";
RL J. Biol. Chem. 270:23726-23729 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";


```
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [3]
RP SEQUENCE OF 2-504 FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawabayashi Y., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (K1AA0041-K1AA0080) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 1:223-229(1994).
CC -!- FUNCTION: BELONGS TO THE 26S MULTISUBUNIT PROTEASE, WHICH IS
CC REQUIRED FOR UBIQUITIN-DEPENDENT PROTEOLYSIS. DOES NOT BIND
CC UBIQUITIN POLYMERS.
CC -!- SUBUNIT: 26S PROTEASE IS COMPOSED OF A MULTICATALYTIC PROTEASE
CC (PROTEASOME) AND A REGULATORY ATPASE COMPLEX. BOTH ARE
CC MULTISUBUNIT STRUCTURES THAT ASSOCIATE IN THE PRESENCE OF ATP TO
CC FORM THE PROTEASE. SUBUNIT S5B IS PART OF THE REGULATORY COMPLEX.
CC -!- DOMAIN: RICH IN DILEUCINE REPEATS, WHICH HAVE BEEN IMPLICATED IN
CC TRAFFICKING OF A VARIETY OF TRANSMEMBRANE PROTEINS.
CC -!- PTM: THE N-TERMINAL IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S5B FAMILY.
CC -----
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CC -----
DR EMBL: S79862; AAB35397.1; -.
DR EMBL: BC014478; AAH14478.1; -.
DR EMBL: D31889; BAA06687.1; -.
DR Genew: HGNC:9563; PSMDS.
DR GK: Q16401; -.
DR MIM: 604452; -.
DR GO: GO:0005837; C:26S proteasome; TAS.
KW Proteasome.
SQ SEQUENCE 504 AA; 56195 MW; 30F31602DDF:EFH9 CRC64;

Query Match 1.7%; Score 7; DB Length 504;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 LDAISSL 335
DB 362 LDAISSL 368
|||||

RESULT 32
SPKD SYN3 ID SPKD SYN3 STANDARD; PRT; 505 AA.
AC PS4735;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine-protein kinase D (EC 2.7.1.37).
GN SPKD OR SL0776.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamei A., Ikeuchi M.;
RT "A novel gene, spkD, encodes active Ser/Thr protein kinase in the
RT motile cyanobacterium Synechocystis sp. PCC 6803.";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiura M., Tabata S.;
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*Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64k to 92k of the genome.*;
RL DNA Res. 2:153-166(1995)
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
DR EMBL: AB046600; BAB17036.1; -.
DR EMBL: D64005; BAA10726.1; -.
DR PIR: S77034; S77034.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR003646; SH3_Bac.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SMO0287; SH3b; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Complete proteome.
FT DOMAIN 9 271 PROTEIN KINASE.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 40 40 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
SQ SEQUENCE 505 AA; 55213 MW; C4F12A1886C4D51C CRC64;

Query Match 1.7%; Score 7; DB 1; Length 505;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGD 138
DB 16 GSGGFGD 22
|||||

RESULT 33
SYK_HALN1 ID SYK_HALN1 STANDARD; PRT; 548 AA.
AC Q9HNN7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine-tRNA ligase) (LysRS).
GN LYSS OR VNG2017G.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laasy S.R., Baliga N.S., Thorson V., Sirogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
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CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; A605095; AAG20183.1; -
DR PIR; C84352; C84352.
DR HAMAP; MF 00177; -; 1.
DR InterPro; IPR002904; Lys tRNA-synt_1c.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF01921; tRNA-synt_1f; 1.
DR TIGRfam; TIGR00467; lysS_arch; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 43 51 "HIGH" REGION.
FT SITE 308 312 "RMSKS" REGION.
SQ SEQUENCE 548 AA: 63874 MW: 850268AC7F7FD48 CRC64;
Query Match 1.7% Score 7; DB 1; Length 548;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 213 VLALLEL 219
DB 322 VLALLEL 328
RESULT 34
E2K2 HUMAN
ID E2K2_HUMAN STANDARD; PRT; 551 AA.
AC 19525;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interferon-induced, double-stranded RNA-activated protein kinase
DE (EC 2.7.1.1) [Interferon-inducible RNA-dependent protein kinase] (p68
DE kinase) (PI)/eIF-2A protein kinase).
DE GN PKR OR EIF2AK2 OR PKR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 101-118 AND 309-325.
RX MEDLINE=90322433; PubMed=1695551;
RA Meurs E., Chong K., Galabru J., Thomas N.S.B., Kerr I.M.,
RA Williams B.R.G., Hovanessian A.G.;
RT "Molecular cloning and characterization of the human double-stranded
RT RNA-activated protein kinase induced by interferon.";
RL Cell 62:379-390(1990).
RN [2]
RP REVISIONS.
RA Meurs E.;
RL Submitted (XXX-1990) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230231; PubMed=1373553;
RA Thomis D.C., Doohan J.P., Samuel C.E.;
RT "Mechanism of interferon action: cDNA structure, expression, and
RT regulation of the interferon-induced, RNA-dependent PI/eIF-2 alpha
RT protein kinase from human cells.";
RL Virology 188:33-46(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96411668; PubMed=8812437;
RA Kuhen K.L., Shen X., Carlisle E.R., Richardson A.L., Weier H.U.G.,

RA Tanaka H., Samuel C.E.;
RT "Structural organization of the human gene (PKR) encoding an
RT interferon-inducible RNA-dependent protein kinase (PKR) and
RT differences from its mouse homolog.";
RL Genomics 36:197-201(1996).
RN [5]
RP MUTAGENESIS AND AUTOPHOSPHORYLATION OF THR-446 AND THR-451.
RX MEDLINE=2136157; PubMed=1137501;
RA Zhang F., Romano P.R., Nagamura-Inoue T., Tian B., Dever T.E.,
RA Mathews M.B., Ozato K., Hinnebusch A.G.;
RT "Binding of double-stranded RNA to protein kinase PKR is required for
RT dimerization and promotes critical autophosphorylation events in the
RT activation loop.";
RL J. Biol. Chem. 276:24946-24958(2001).
RN [6]
RP STRUCTURE BY NMR OF 1-175.
RX MEDLINE=98409549; PubMed=9736623;
RA Nanduri S., Carpick B.W., Yang Y., Williams B.R., Qin J.;
RT "Structure of the double-stranded RNA-binding domain of the protein
RT kinase PKR reveals the molecular basis of its dsRNA-mediated
RT activation.";
RL EMBL J. 17:5458-5465(1998).
CC -!- FUNCTION: ON ACTIVATION BY DOUBLE-STRANDED RNA IN THE PRESENCE OF
CC ATP, THE KINASE BECOMES AUTOPHOSPHORYLATED AND CAN CATALYZE THE
CC PHOSPHORYLATION OF THE ALPHA SUBUNIT OF EIF2, WHICH LEADS TO AN
CC INHIBITION OF THE INITIATION OF PROTEIN SYNTHESIS.
CC -!- ENZYME REGULATION: Activity is markedly stimulated by manganese
CC ions. Besides dsRNA, hepari is a potent activator of the kinase.
CC Binding to dsRNA is require for dimerization leading to
CC autophosphorylation in the ctivation loop and stimulation of
CC function.
CC -!- SUBUNIT: Homodimer.
CC -!- INDUCTION: By interferon.
CC -!- PTM: Autophosphorylated on several Ser and Thr residues.
CC Autophosphorylation of Thr-451 is dependent on Thr-446 and is
CC stimulated by dsRNA binding and dimerization.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC GCN2 SUBFAMILY.
CC -!- SIMILARITY: Contains 2 DBRM (double-stranded RNA-binding) domains.
CC -----
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CC -----
DR EMBL; M35663; AAA36409.1; -
DR EMBL; M85294; AAA18253.1; -
DR EMBL; U50648; AAC50768.1; -
DR EMBL; U50634; AAC50768.1; JOINED.
DR EMBL; U50635; AAC50768.1; JOINED.
DR EMBL; U50636; AAC50768.1; JOINED.
DR EMBL; U50637; AAC50768.1; JOINED.
DR EMBL; U50638; AAC50768.1; JOINED.
DR EMBL; U50639; AAC50768.1; JOINED.
DR EMBL; U50640; AAC50768.1; JOINED.
DR EMBL; U50641; AAC50768.1; JOINED.
DR EMBL; U50642; AAC50768.1; JOINED.
DR EMBL; U50643; AAC50768.1; JOINED.
DR EMBL; U50644; AAC50768.1; JOINED.
DR EMBL; U50645; AAC50768.1; JOINED.
DR EMBL; U50646; AAC50768.1; JOINED.
DR EMBL; U50647; AAC50768.1; JOINED.
DR PIR; JCS225; JCS225.
DR PDB; 1QU6; 23-DEC-99.
DR Genew; HGNC:9437; PKR.
DR MIM; 176871; -
DR GO; GO:0003725; F:double-stranded RNA binding activity; TAS.
DR GO; GO:0004694; F:eukaryotic translation initiation factor 2a.; TAS.
DR GO; GO:0008601; F:protein phosphatase type 2A, regulator acti.; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

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DR GO: 0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro: IPR001159; DS RBD.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00035; dsrm; 2.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00358; DSRM; 2.
DR PROSITE: PS00137; DS_RBD; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR Transferase: Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Phosphorylation; Interferon induction; RNA-binding; 3D-structure.
FT DOMAIN 59 75
FT DOMAIN 149 165
FT DOMAIN 267 538
FT NP_BIND 273 281
FT BINDING 296 296
FT ACT_SITE 414 414
FT DOMAIN 331 357
FT REPEAT 331 343
FT REPEAT 345 357
FT MOD_RES 446 446
FT MOD_RES 451 451
FT MUTAGEN 59 60
FT MUTAGEN 60 60
FT MUTAGEN 67 67
FT MUTAGEN 149 150
FT MUTAGEN 244 296
FT MUTAGEN 258 258
FT MUTAGEN 296 296
FT MUTAGEN 446 446
FT MUTAGEN 451 451
FT SEQUENCE 551 AA; 62094 MW; 815AD83ACAB45DA3 CRC64;

Query Match 1.7%; Score 7; DB 1 Length 551;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFG 137
Db 273 IGSGGFG 279

RESULT 35
GGT_PSESP
ID_GGT_PSESP STANDARD; PRT; 575 AA.
AC P36267;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2).
GN GGT.
OS Pseudomonas sp. (strain A14).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=93305254; PubMed=7765305;
RA Iehiye M., Yamashita M., Niwa M.;
RT "Molecular cloning of the gamma-glutamyltranspeptidase gene from a
RT Pseudomonas strain."
RL Biotechnol. Prog. 9:323-331(1993).
CC -!- CATALYTIC ACTIVITY: (S-L-glutamyl)-peptide + an amino acid =
CC peptide + S-L-glutamyl-amino acid.

GO: 0006468; P:protein amino acid phosphorylation; TAS.
-!- PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, A
-!- PATHWAY FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.
-!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH ARE
-!- SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE.
-!- SUBCELLULAR LOCATION: Periplasmic (BY SIMILARITY).
-!- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
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EMBL: S63255; AAC60442.1; -.
DR MEROPS: T03.001; -.
DR InterPro: IPR000101; Gglutnspptase.
DR Pfam: PF01019; Gglu_transpept; 1.
DR PRINTS: PR01210; GGTTRANSPTASE.
DR TIGRFAMs: TIGR00066; gglu_trans; 1.
DR PROSITE: PS00462; G_GLU_TRANSPEPTIDASE; 1.
KW Transferase; Acyltransferase; Periplasmic; Zymogen; Signal;
KW Glutathione biosynthesis.
FT SIGNAL 1 24
FT CHAIN 25 376
FT CHAIN 377 575
FT BINDING 450 450
FT SEQUENCE 575 AA; 61301 MW; CF2EB69F02CD0201 CRC64;

Query Match 1.7%; Score 7; DB 1 Length 575;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 PSLGGKP 279
Db 547 PSLGGKP 553

RESULT 36
LU_HUMAN
ID_LU_HUMAN STANDARD; PRT; 628 AA.
AC P50895;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lutheran blood group glycoprotein precursor (B-CAM cell surface
DE glycoprotein) (Aubberger B antigen) (F8/G253 antigen).
GN LU OR BCAM OR MSK19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 32-67 AND 182-203.
RC TISSUE=Placenta;
RX MEDLINE=95296337; PubMed=7777537;
RA Parsons S.F., Mallinson G., Holmes C.H., Houlihan J.M., Simpson K.L.,
RA Mawby W.J., Spurr N.K., Warne D., Barclay A.N., Anstee D.J.;
RT "The Lutheran blood group glycoprotein, another member of the
RT immunoglobulin superfamily, is widely expressed in human tissues and
RT is developmentally regulated in human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 92:5496-5500(1995).
RN [2]
RP SEQUENCE OF 1-588 FROM N.A.
RX MEDLINE=95042297; PubMed=7954395;
RA Campbell I.G., Foulkes W.D., Senger G., Trowsdale J.,
RA Garin-Chesa P., Rettig W.J.;
RT "Molecular cloning of the B-CAM cell surface glycoprotein of
RT epithelial cancers: a novel member of the immunoglobulin
RT superfamily."
RL Cancer Res. 54:5761-5765(1994).
CC -!- FUNCTION: PROBABLE RECEPTOR. MAY MEDIATE INTRAELULAR SIGNALING.

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RX MEDLINE-92033088; PubMed-1932811;
RA Camilleri C., Jouanin L.;
RT "The TR-DNA region carrying the auxin synthesis genes of the
RT Agrobacterium rhizogenes agropine-type plasmid pRIA4: nucleotide
RT sequence analysis and introduction into tobacco plants.";
RL Mol. Plant Microbe Interact. 4:155-162(1991).
CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.
CC -!- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
CC -----
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CC -----
CC EMBL; M61151; AAA22080.1; -
CC PIR; I39708; I39708.
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR002937; Amino_oxidase.
CC InterPro; IPR006064; Glycosidase.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF01593; Amino_oxidase; 1.
CC Pfam; PF02027; RolB_RolC; 1.
CC PRINTS; PR00419; ADXRDTASE.
CC Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
KW T-DNA; Plasmid.
KW Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
FT VARIANT 718 719 721 NR -> IQ (IN PTIA6NC).
FT VARIANT 721 721 P -> A (IN PTIA6NC).
SQ SEQUENCE 749 AA; 83178 MW; 8B77939702C7B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 749;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFG 137
DB 421 IGSGGFG 427

RESULT 39
TR2M_AGR4
ID TR2N_AGRV1 STANDARD; PRT; 755 AA.
AC P25017;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN TMS1
OS Agrobacterium tumefaciens (strain Ach5), and
OS Agrobacterium tumefaciens.
OG Plasmid pTIAch5, and Plasmid pTIA6NC.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176298, 358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ach5;
RX MEDLINE-84207942; PubMed=6327292;
RA Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
RA Lemmers M., van Montagu M., Schell J.;
RT "The complete nucleotide sequence of the TL-DNA of the Agrobacterium
RT tumefaciens plasmid pTIAch5.";
RL EMBO J. 3:835-846(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=pTIA6NC.
RX MEDLINE-84170374; PubMed=6584906;
RA Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
RA Fuller S., Flores C., Peschon J., Nester E., Gordon M.;
RT "Nucleotide sequence of the tms genes of the pTIA6NC octopine Ti
RT plasmid: two gene products involved in plant tumorigenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).
CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +

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CC CO(2) + H(2)O.
CC -!- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.
CC -!- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF
CC P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT
CC THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02554; AAA92550.1; -
CC PIR; A04497; QOAG47.
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR002937; Amino_oxidase.
CC InterPro; IPR006064; Glycosidase.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF01593; Amino_oxidase; 1.
CC Pfam; PF02027; RolB_RolC; 1.
CC PRINTS; PR00419; ADXRDTASE.
CC Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
KW T-DNA; Plasmid.
KW Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
FT VARIANT 718 719 721 NR -> IQ (IN PTIA6NC).
FT VARIANT 721 721 P -> A (IN PTIA6NC).
SQ SEQUENCE 755 AA; 83947 MW; 9FD2B83FEA001A4D CRC64;

Query Match 1.7%; Score 7; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFG 137
DB 436 IGSGGFG 442

RESULT 40
TR2N_AGRV1
ID TR2N_AGRV1 STANDARD; PRT; 755 AA.
AC P25017;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
GN IAAH.
OS Agrobacterium vitis (Rhizobium vitis).
OG Plasmid pTITM4.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TM4;
RX MEDLINE=91329707; PubMed=1868204;
RA Bonnard G., Vincent F., Otten L.;
RT "Sequence of Agrobacterium tumefaciens biotype III auxin genes.";
RL Plant Mol. Biol. 16:733-738(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CG474;
RX OTTEN L., de RUFFRAY P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.
CC -!- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
CC -!- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF
CC P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT
CC THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC -!- SIMILARITY: STRONG, WITH ITS COUNTERPARTS FROM A. TUMEFACIENS
CC PLASMIDS PTI15955, PTIACH5 AND PTIA6NC.

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EMBL; AP005375; BAC09464.1; --
 DR EMBL; AB057454; BAB64533.1; --
 DR HAMAP; MF 00595; -- 1.
 DR InterPro; IPR001449; PEPcase.
 DR Pfam; PF00311; PEPcase; 1.
 DR PRINTS; PR00150; PEPCARBLASE.
 DR PROSITE; PS00781; PEPcase 1; FALSE_NEG.
 DR PROSITE; PS00393; PEPcase 2; 1.
 KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
 KW Complete proteome.
 FT ACT_SITE 207 BY SIMILARITY.
 FT ACT_SITE 658 BY SIMILARITY.
 FT ACT_SITE 658 BY SIMILARITY.
 SQ SEQUENCE 1011 AA; 116426 MW; 0A11D4D01FE9E7FE CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1011;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RLRLVEE 19
 DB 27 RLRLVEE 33

RESULT 43

UL70_HCMVA STANDARD; PRT; 1062 AA.
 ID UL70_HCMVA
 AC P17149;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Helicase/primase complex protein (Probable DNA replication protein
 DE UL70).
 GN UL70.
 OS Human cytomegalovirus (strain AD169).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OC NCBI_TaxID=10360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90269039; PubMed=2161319;
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Horsnell T., Hutchinson C.A. III, Kourazides T., Martignetti J.A.,
 RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RA "Analysis of the protein-coding content of the sequence of human
 RT cytomegalovirus strain AD169.";
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 CC -!- FUNCTION: INVOLVED IN DNA REPLICATION
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,
 CC EBV-1 7, EBV BSLF1, HVS-1 56, HCMV UL70 AND VZV 6.

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EMBL; X17403; CAA35386.1; --
 DR PIR; S09834; S09834.
 DR InterPro; IPR004340; UL52 UL70.
 DR Pfam; PF03121; UL52_UL70; 1.
 KW DNA replication.
 SQ SEQUENCE 1062 AA; 120925 MW; F3B8DBC29857524F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 VASTSPE 304
 DB 604 VASTSPE 610

RESULT 44

Y056_HUMAN STANDARD; PRT; 1507 AA.
 ID Y056_HUMAN
 AC P42695;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein KIAA0056 (Fragment).
 GN KIAA0056.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=96051398; PubMed=7584044;
 RA Nomura N., Nagase T., Miyajima T., Suzuki T., Tanaka A., Sato S.,
 RA Seki N., Kawabayashi Y., Ishikawa K.-I., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. II.
 RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 1:223-229(1994).
 RN [2]
 RP SEQUENCE OF 1171-1507 FROM N.A.
 RC TISSUE=Brain;
 RA Yu W.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.

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EMBL; D29954; BAA06224.1; --
 DR EMBL; AF070553; AAC28639.1; --
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 1507 AA; 169717 MW; D56BCA948FE927D2 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1507;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 VLALLEL 219
 DB 425 VLALLEL 431

RESULT 45

OTOF_HUMAN STANDARD; PRT; 1997 AA.
 ID OTOF_HUMAN
 AC Q9HC10; Q9HC08; Q9HC09; Q9Y650;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ocoferlin (fer-1 like protein 2).
 GN OTOF OR FER1L2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RC MEDLINE=20395831; PubMed=10903124;
 RA Yasunaga S., Grati M., Chardenoux S., Smith T.N., Friedman T.B.,
 RA Lalwai A.K., Wilcox E.R., Petit C.;
 RT "OTOF encodes multiple long and short isoforms: genetic evidence that
 RT the long ones underlie recessive deafness DFNB9.";
 RL Am. J. Hum. Genet. 67:591-600(2000).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Fetal;
 RC MEDLINE=95206603; PubMed=10192385;
 RA Yasunaga S., Grati M., Cohen-Salmon M., El-Amraoui A., Mustapha M.,
 RA Salem N., El-Zir E., Loiselet J., Petit C.;
 RT "A mutation in OTOF, encoding otoferlin, a PER-1-like protein, causes
 RT DFNB9, a nonsyndromic form of deafness.";
 RL Nat. Genet. 21:363-369(1999).
 CC -1- FUNCTION: Might be involved in the Ca(2+)-triggered synaptic
 CC vesicle-plasma membrane fusion.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q9HC10-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short-1;
 CC IsoId=Q9HC10-2; Sequence=VSP_001507, /SP_001508, VSP_001511;
 CC Name=3; Synonyms=Short-2;
 CC IsoId=Q9HC10-3; Sequence=VSP_001509, /SP_001510;
 CC Name=4; Synonyms=Short-3;
 CC IsoId=Q9HC10-4; Sequence=VSP_001507, VSP_001508;
 CC -1- TISSUE SPECIFICITY: Isoform 1 and isoform 3 are found in adult
 CC brain. Isoform 2 is expressed in the fetus and in adult brain,
 CC heart, placenta, skeletal muscle and kidney.
 CC -1- DISEASE: Defects in OTOF are the cause of nonsyndromic autosomal
 CC recessive deafness 9 (DFNB9).
 CC -1- SIMILARITY: BELONGS TO THE PERLIN FAMILY.
 CC -1- SIMILARITY: Contains 4 C2 domains.
 CC -----
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 CC -----
 DR EMBL; AF183185; AAG12991.1; -;
 DR EMBL; AF183186; AAG12992.1; -;
 DR EMBL; AF183187; AAG17468.1; -;
 DR EMBL; AF107403; AAD26117.1; -;
 DR HSP; P04410; IAA25.
 DR Genew; HGNC:8515; OTOF.
 DR MIM; 603681; -;
 DR MIM; 601071; -;
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 7.
 DR PRINTS; PR00360; C2DOMAIN.
 DR SMART; SM00239; C2; 6.
 DR PROSITE; PS00499; C2_DOMAIN_1; 2.
 DR PROSITE; PS00004; C2_DOMAIN_2; 4.
 DR Transmembrane; Repeat; Alternative splicing; Deafness.
 FT DOMAIN 1 1963 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 1964 1984 POTENTIAL.
 FT DOMAIN 1985 1997 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 241 338 C2 DOMAIN 1.
 FT DOMAIN 404 514 C2 DOMAIN 2.
 FT DOMAIN 947 1052 C2 DOMAIN 3.
 FT DOMAIN 1479 1577 C2 DOMAIN 4.
 FT DOMAIN 1303 1310 POLY-LYS.
 FT DOMAIN 1314 1320 POLY-GLU.

FT DOMAIN 1965 1983 POLY-LEU.
 FT VARSPLIC 1 747 Missing (in isoform 2 and isoform 4).
 FT VARSPLIC 1245 1264 /FTId=VSP_001507.
 FT VARSPLIC 1 690 Missing (in isoform 2 and isoform 4).
 FT VARSPLIC 691 738 /FTId=VSP_001508.
 FT VARSPLIC 691 738 Missing (in isoform 3).
 FT VARSPLIC 691 738 /FTId=VSP_001509.
 FT VARSPLIC 691 738 MRPOVTDNRYFHLPLVLERKPCYIKSWPDDORRLYNANIM
 FT VARSPLIC 691 738 DHIADKL -> MWTDIQGPSSSOIMBSLTLLINREAFG
 FT VARSPLIC 691 738 EAGEAGLWPSITHTPDSQ (in isoform 3).
 FT VARSPLIC 691 738 /FTId=VSP_001510.
 FT VARSPLIC 691 738 SFWFLNPLKRSARYFLMHTYRWLLKLLLLLLLLLLLALFL
 FT VARSPLIC 691 738 YSVGFLVKKILGA -> AFVWFLNPLKRSIKYIKTRYKWL
 FT VARSPLIC 691 738 IIKVILALGLMLGLFLYSLPGYMKVKKLLGA (in
 FT VARSPLIC 691 738 isoform 2).
 FT VARSPLIC 691 738 /FTId=VSP_001511.
 FT VARSPLIC 691 738 P -> L (IN REF 1; AAG12991).
 FT VARSPLIC 691 738 SEQUENCE 1997 AA; 226735 MW; 39D10CRS220638AE CRC64;
 SQ SEQUENCE 1997 AA; 226735 MW; 39D10CRS220638AE CRC64;
 Query Match. 1.7%; Score 7; DB 1; Length 1997;
 Best Local Similarity 100.0%; Pred. No. 2.3e-02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 RLRRRCR 13
 Db 1246 RLLRRRCR 1252
 RESULT 46
 CAIC_MOUSE
 ID CAIC_MOUSE STANDARD; PRT; 3119 AA.
 AC Q60847; P70322;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(XII) chain precursor.
 GN COL12A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-1 AND
 RN XIIB-1).
 RC STRAIN=Swiss Webster, and C57BL/6J; TISSUE=Skin;
 RC MEDLINE=96170761; PubMed=8601036;
 RA Boehme K., Li Y., Oh P.S., Olsen B.R.;
 RT "Primary structure of the long and short splice variants of mouse
 RT collagen XII and their tissue-specific expression during embryonic
 RT development.";
 RL Dev. Dyn. 204:432-445(1995).
 RN [2]
 RN PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-2
 RN AND XIIB-2).
 RC STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
 RC MEDLINE=99348349; PubMed=10419532;
 RA Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W.,
 RA Olsen B.R., Nishimura I.;
 RT "Structural variation of type XII collagen at its carboxyl-terminal
 RT NC1 domain generated by tissue-specific alternative splicing.";
 RL J. Biol. Chem. 274:22053-22059(1999).
 CC -1- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
 CC CONTAINING FIBRILS, THE COL1 DOMAIN COULD BE ASSOCIATED WITH THE
 CC SURFACE OF THE FIBRILS, AND THE COL2 AND NC3 DOMAINS MAY BE
 CC LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).
 CC -1- SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 KDa OF
 CC NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=The final tissue form of collagen XII may contain
 CC homotrimers or any combination of the various isoforms;
 CC Name=XIIA-1;
 CC IsoId=Q60847-1; Sequence=Displayed;

CC Name=XIIA-2; Synonym=ERR#K;
 CC IsoId=060847-2; Sequence=VSP_001151, VSP_001152;
 CC Name=XIIB-1;
 CC IsoId=060847-3; Sequence=VSP_001150;
 CC Name=XIIB-2;
 CC IsoId=060847-4; Sequence=VSP_001150, VSP_001151, VSP_001152;
 CC TISSUE SPECIFICITY: HIGHEST EXPRESSION N TENDONS, PERICHOONDRIUM,
 CC SKIN, CORNEA, SCLERA, BLOOD VESSELS, ANJ PERIOSTEUM.
 CC EARLY DEVELOPMENTAL STAGE: THE LONG NC3 XIIA ISOFORMS ARE PREDOMINANT AT
 CC AND 17) THE SHORT NC3 XIIB FORMS BECOME THE MAJOR PRODUCTS. AS THE
 CC SHORT NC3 FORMS BECOME THE MAJOR PRODUCTS, THE LONG SPLICE VARIANT
 CC CONTINUES TO BE EXPRESSED IN SEVERAL TISSUES, EVEN AFTER BIRTH.
 CC THE LONG NC1 ISOFORMS, XIIA-1 AND XIIB-1, PEAK IN 15-DAY OLD
 CC EMBRYOS AND DECREASE IN 17-DAY OLD ONES. THE EXPRESSION OF THE
 CC SHORT NC1 FORM XIIB-2 REMAINS CONSTANT THROUGHOUT LATE STAGES OF
 CC EMBRYONIC DEVELOPMENT (ED15 AND ED17).
 CC PTM: The triple-helical tail is stabilized by disulfide bonds at
 CC each end (BY similarity).
 CC PTM: Prolines at the third position of the tripeptide repeating
 CC unit (G-X-Y) are hydroxylated in some or all of the chains (BY
 CC similarity).
 CC PTM: O-glycosylation of isoform XIIA-2; glycosaminoglycan of
 CC chondroitin-sulfate type (BY similarity).
 CC SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
 CC INTERRUPTED HELICES (FACIT) FAMILY.
 CC SIMILARITY: Contains 4 VWFA domains.
 CC SIMILARITY: Contains 18 fibronectin type III domains.
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 CC EMBL; U25652; AAA99719.1; ALT_SEQ.
 DR EMBL; U57095; AAB07047.1;
 DR HSPSP; P02751; IFNA.
 DR MGD; MGI:88448; Coll2a1.
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01391; Collagen_5.
 DR Pfam; PF00041; fn3; 18.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00092; vwa; 4.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00060; FN3; 18.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00327; VWA; 4.
 DR PROSITE; PS50234; VWFA; 4.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 3119 COLLAGEN ALPHA 1(XII) CHAIN.
 FT DOMAIN 25 114 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 140 316 VWFA 1.
 FT DOMAIN 332 423 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 444 620 VWFA 2.
 FT DOMAIN 634 725 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 726 816 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 817 907 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 908 1002 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 1003 1089 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1203 1375 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1368 1474 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1480 1568 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1549 1652 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1659 1757 FIBRONECTIN TYPE-III 12.

FT DOMAIN 1758 1848 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1849 1938 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1939 2029 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2030 2120 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 2121 2208 FIBRONECTIN TYPE-III 17.
 FT DOMAIN 2209 2297 FIBRONECTIN TYPE-III 18.
 FT DOMAIN 2329 2501 VWFA 4.
 FT DOMAIN 2456 2751 NONHELICAL REGION (NC3).
 FT DOMAIN 2752 2899 TRIPLE-HELICAL REGION (COL2) WITH 1 IMPERFECTION.
 FT DOMAIN 2900 2942 NONHELICAL REGION (NC2).
 FT DOMAIN 2943 3045 TRIPLE-HELICAL REGION (COL1) WITH 2 IMPERFECTIONS.
 FT DOMAIN 3046 3119 NONHELICAL REGION (NC1).
 FT SITE 866 868 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 2784 2786 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 2896 2898 CELL ATTACHMENT SITE (POTENTIAL).
 FT MOD_RES 2945 2945 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2948 2948 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2951 2951 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2960 2960 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2966 2966 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2969 2969 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2972 2972 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 2984 2984 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3001 3001 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3004 3004 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3015 3015 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3024 3024 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3027 3027 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 3030 3030 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 869 872 POLY-THR.
 FT CARBOHYD 704 704 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 802 802 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 FT CARBOHYD 893 893 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 FT CARBOHYD 985 985 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 FT CARBOHYD 1769 1769 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2212 2212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2684 2684 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 25 1190 Missing (in isoform XIIB-1 and isoform XIIB-2).
 FT VARSPLIC 3062 3064 /FTID=VSP 001150.
 FT VARSPLIC 3065 3119 EPI -> GSG (in isoform XIIA-2 and isoform XIIB-2).
 FT VARSPLIC 3065 3119 /FTID=VSP 001151.
 FT VARSPLIC 3065 3119 Missing (in isoform XIIA-2 and isoform XIIB-2).
 FT VARSPLIC 3065 3119 /FTID=VSP 001152.
 SQ SEQUENCE 3119 AA; 340239 MW; 9B1F999C86AB3251 CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 3119;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 102 TLENLTP 108
 Db 782 TLENLTP 788
 RESULT 47
 GIAN HUMAN STANDARD; PRT; 3259 AA.
 ID Q14789; Q14398;
 AC Q14789; Q14398;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Golgi autoantigen, golgin subfamily B member 1 (Giantin) (Macroglolin)
 DE (Golgi complex-associated protein, 372-kDa) (GCP372).
 GN GOLGB1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187728; PubMed=7511208;
 RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
 RA Renz M.;
 RT "Molecular genetic analyses of a 376-kilodalton Golgi complex membrane
 RL protein (giantin).";
 RL Mol. Cell. Biol. 14:2564-2576(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94257116; PubMed=8198703;
 RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
 RA Renz M.;
 RT "Macrogolgin -- a new 376 kD Golgi complex outer membrane protein as
 RT target of antibodies in patients with rheumatic diseases and HIV
 RL infections.";
 RL J. Autoimmun. 7:67-9;(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95100974; PubMed=7802676;
 RA Sohma M., Misumi Y., Fujiwara T., Nishioka M., Ikehara Y.;
 RT "Molecular cloning and sequence analysis of a human 372-kDa protein
 RL localized in the Golgi complex";
 RL Biochem. Biophys. Res. Commun. 205:1399-1408(1994).
 CC -|- FUNCTION: May participate in forming intercisternal cross-bridges
 CC of the Golgi complex.
 CC -|- SUBUNIT: Homodimer; disulfide-linked.
 CC -|- SUBCELLULAR LOCATION: Membrane-associated protein. Golgi.
 CC -|- DISEASE: Antigen in chronic rheumatoid arthritis and in the
 CC autoimmune disease Sjogren's syndrome.
 CC
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 CC
 DR EMBL; X75304; CAA35052.1; -;
 DR EMBL; D25542; BAA05025.1; -;
 DR PIR; A56539; A56539.
 DR PIR; I52300; I52300.
 DR Genew; HGNC:4429; GOLGB1.
 DR MTM; 602500; -;
 DR GO; GO:0000139; C:Golgi membrane; TAS.
 DR GO; GO:0005795; C:Golgi stack; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0007030; P:Golgi organization and biogenesis; TAS.
 KW Golgi stack; Antigen; Coiled coil; Transmembr.
 FT DOMAIN 1 3235 CYTOPLASMIC (POT. IAL).
 FT TRANSMEM 3236 3256 POTENTIAL.
 FT DOMAIN 3257 3259 LUMENAL (POTENTIAL).
 FT DOMAIN 48 593 COILED COIL (POTENTIAL).
 FT DOMAIN 677 1028 COILED COIL (POTENTIAL).
 FT DOMAIN 1062 1245 COILED COIL (POTENTIAL).
 FT DOMAIN 1301 1779 COILED COIL (POTENTIAL).
 FT DOMAIN 1828 3185 COILED COIL (POTENTIAL).
 FT DOMAIN 2420 2423 POLY-GLU.
 FT DOMAIN 2993 2996 POLY-SER.
 FT CONFLICT 1 39 MISSING (IN REF. 3).
 FT CONFLICT 215 215 A -> AQLSSM (IN REF. 3).
 FT CONFLICT 1765 1765 D -> G (IN REF. 3).
 FT CONFLICT 2950 2950 H -> D (IN REF. 3).
 SQ SEQUENCE 3259 AA; 376075 MW; 60376A20D8A1 3D CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 3259;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 77 LEDTQD 83
 DB 615 LEDTQD 621
 RESULT 48
 AT12 HSVB4
 ID AT12 HSVB4 STANDARD; PRT; 45 AA.
 AC Q00041;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Alpha trans-inducing factor 82 kDa protein (Fragment).
 GN 14 OR B7.
 OS Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus
 OS type 1 subtype 2).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10333;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91202570; PubMed=1850013;
 RA Whittaker G.R., Riggio M.P., Halliburton I.W., Killington R.A.,
 RA Allen G.P., Meredith D.M.;
 RT "Antigenic and protein sequence homology between VP13/14, a herpes
 RT simplex virus type 1 tegument protein, and gp10, a glycoprotein of
 RT equine herpesvirus 1 and 4";
 RL J. Virol. 65:2320-2326(1991).
 CC -|- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
 CC ACTIVATION OF ALPHA GENES (BY SIMILARITY).
 CC
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 CC
 DR EMBL; X17684; CAA35673.1; -;
 DR PIR; S36709; S36709.
 DR InterPro; IPR005051; Herpes UL46.
 DR Pfam; PF03387; Herpes UL46; 1.
 KW Transcription regulation; Trans-acting factor.
 FT NON_TER 45 45
 SQ SEQUENCE 45 AA; 4862 MW; AAE468C9C2B08BE4 CRC64;
 Query Match 1.4%; Score 6; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 335 LPTPSD 340
 DB 27 LPTPSD 32
 RESULT 49
 GON1 MACMU
 ID GON1 MACMU STANDARD; PRT; 67 AA.
 AC P55247;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I]
 DE (Fragment)
 GN GNRH1 OR GNRH OR LHRH.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.

```

OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=95124501; PubMed=7545971;
RA Ma Y.J., Costa M.E., Ojeda S.R.;
RT "Developmental expression of the genes encoding transforming growth
RT factor alpha and its receptor in the hypothalamus of female rhesus
RT macaques.";
RL Neuroendocrinology 60:346-359(1994).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
CC THE SECRETION OF BOTH LUTEINIZING AND FOLLICUL-STEMULATING
CC HORMONES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
CC -----
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CC -----
DR EMBL: S75918; AAB33096.1;
DR PIR: I78541; I78541.
DR InterPro: IPR002012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR PRINTS: PR01541; GONADOLIBRN1.
DR PROSITE: PS00473; GNRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KM Signal; Pyrrolidone carboxylic acid.
FT NON_TER 1
FT SIGNAL <1 5
FT CHAIN 6 >67
FT PEPTIDE 6 15
FT PEPTIDE 19 >67
FT ACT_SITE 8
FT MOD_RES 6 6
FT MOD_RES 15 15
FT NON_TER 67
FT SEQUENCE 67 AA; 7573 MW; 505394DAA261A3F2 CRC64;

Query Match 1.48; Score 6; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 GALESL 145
Db 59 GALESL 64
|||||

RESULT 50
YQKK_BACSU
ID YQKK_BACSU STANDARD; PRT; 71 AA.
AC P54573;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yqkk.
GS YQKK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273731; PubMed=8501064;
RA Smith K., Bayer M.E., Youngman P.;
RT "Physical and functional characterization of the Bacillus subtilis

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RT spoliim gene.";
RL J. Bacteriol. 175:3607-3617(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes.";
RL Microbiology 142:3103-3111(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchart S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusier C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dueterhoff A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kunano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Preecan E., Puic P., Putnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Soldo B.,
RA Sekiguchi J., Sakowska A., Saror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Totsu T., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viati A., Wambutt R., Wedler E., Wedler H., Weitzmeger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06664; -: NOT ANNOTATED_CDS.
DR EMBL: D84432; BAA12646.1;
DR EMBL: Z99116; CAB14286.1;
DR PIR: D69967; D69967.
DR Subtilist; Bg11765; yqkk.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 71 AA; 8090 MW; 826426E143027A03 CRC64;

Query Match 1.48; Score 6; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 DVLRSR 32
Db 20 DVLRSR 25

```

Mon Oct 20 12:22:51 2003

us-09-961-201a-1.oligo.rsp

Pag 34

Search completed: October 20, 2003, 12:25:20
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2003, 12:22:07 ; Search time 41 Seconds
(without alignments)
975.760 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 416
Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCCFNLRKLFKTS 416

Scoring table: CLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283108 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	416	100.0	416	2	G02635
2	28	6.7	454	2	JC7123
3	9	2.2	370	2	B88455
4	9	2.2	1396	2	T09356
5	8	1.9	232	2	A69501
6	8	1.9	324	2	AE3650
7	8	1.9	368	2	T36004
8	8	1.9	372	2	G82328
9	8	1.9	579	2	T45344
10	8	1.9	752	2	T16508
11	8	1.9	758	2	T16800
12	8	1.9	787	2	T00798
13	8	1.9	794	2	T23048
14	8	1.9	1393	2	E72122
15	8	1.9	1393	2	B86501
16	8	1.9	1397	2	E81548
17	7	1.7	98	2	AE2465
18	7	1.7	132	2	T44759
19	7	1.7	135	2	B92118
20	7	1.7	173	2	H90776
21	7	1.7	180	2	D86609
22	7	1.7	180	2	E72014
23	7	1.7	180	2	F71056
24	7	1.7	182	2	D75088
25	7	1.7	182	2	G71411
26	7	1.7	186	2	S75396
27	7	1.7	189	2	F82448
28	7	1.7	200	2	G82270
29	7	1.7	206	2	AF2299

30	7	1.7	224	2	E83859	hypothetical prote
31	7	1.7	234	2	T51025	hypothetical prote
32	7	1.7	236	2	T13312	hypothetical prote
33	7	1.7	237	2	G84678	probable RING zinc
34	7	1.7	240	2	D87435	transcription regu
35	7	1.7	241	2	H72691	probable hexulose-
36	7	1.7	247	2	C82995	two-component resp
37	7	1.7	261	2	E69455	conserved hypothet
38	7	1.7	262	2	T18886	hypothetical prote
39	7	1.7	267	2	T06613	hypothetical prote
40	7	1.7	274	2	JQ6686	nosinpeptide resist
41	7	1.7	276	2	T36288	probable ABC-type
42	7	1.7	276	2	E87682	methylytransferase,
43	7	1.7	285	2	B97536	ATP/GTP-binding pr
44	7	1.7	294	2	G71276	conserved hypothet
45	7	1.7	306	2	JC1120	sdeB protein - Pae
46	7	1.7	307	2	D75447	ABC transporter, A
47	7	1.7	311	1	G64456	conserved hypothet
48	7	1.7	313	2	S60713	polygalacturonase-
49	7	1.7	318	2	AB0350	probable membrane
50	7	1.7	319	2	A72637	hypothetical prote
51	7	1.7	323	2	G83461	hypothetical prote
52	7	1.7	329	2	T30513	hypothetical prote
53	7	1.7	333	2	AH0272	conserved hypothet
54	7	1.7	336	2	AF2085	transcription regu
55	7	1.7	345	2	H72488	probable anthranil
56	7	1.7	349	2	AC0856	conserved hypothet
57	7	1.7	358	2	H71058	hypothetical prote
58	7	1.7	358	2	H90052	conserved hypothet
59	7	1.7	360	2	A83004	conserved hypothet
60	7	1.7	361	2	B70189	rod shape-determin
61	7	1.7	379	2	H87268	hypothetical prote
62	7	1.7	388	2	G90450	hypothetical prote
63	7	1.7	390	2	D82186	beta-lactamase-rel
64	7	1.7	397	2	T23026	hypothetical prote
65	7	1.7	401	2	S59670	hypothetical prote
66	7	1.7	404	2	S45923	RAD17 protein - ye
67	7	1.7	420	2	A47649	probable phosphopa
68	7	1.7	420	2	E95982	probable inner mem
69	7	1.7	444	2	AC2755	probable transport
70	7	1.7	487	1	VZEBPT	GTP-binding protei
71	7	1.7	487	2	AG0646	sensor kinase phoQ
72	7	1.7	496	2	F84664	sensor protein pho
73	7	1.7	505	1	S77034	hypothetical prote
74	7	1.7	505	2	AC3361	protein kinase pkn
75	7	1.7	508	2	B01212	GTP-binding protei
						fatty aci: efflux

ALIGNMENTS

RESULT 1

G02635 ICE-LAP6 - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C;Accession: G02635

R;Duan, H.; Orth, K.; Chinraiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,

submitted to the EMBL Data Library, April 1996

A;Reference number: H01513

A;Accession: G02635

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-416 <DUA>

A;Cross-references: EMBL:U56390; NID:1336026; PIDN:AAC50640.1; PID:g1336027

Query Match 100.0%; Sc re 416; DB 2; Length 416;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQDVLRLFRPHMIEDIQAGSGSRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVEELQDVLRLFRPHMIEDIQAGSGSRDQARQLII 60

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OY 61 DLETRGSQLPLFISCLDGTQDMILASFLTRNRQAGKLSKPTLENLTTPVLRPEIRKPEV 120
|||||
Db 61 DLETRGSQLPLFISCLDGTQDMILASFLTRNRQAGKLSKPTLENLTTPVLRPEIRKPEV 120
|||||

OY 121 LRPETPRPVDIGSGGFGDVGALSGRNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
|||||
Db 121 LRPETPRPVDIGSGGFGDVGALSGRNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
|||||

OY 181 TGSNDICEKLRFRFSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
|||||
Db 181 TGSNDICEKLRFRFSLHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
|||||

OY 241 ASHLQFPGAVGTDCGCVSVKIVNIFNGTSCPSLGGKPKLFFTOACGEGEKDHGFEVAS 300
|||||
Db 241 ASHLQFPGAVGTDCGCVSVKIVNIFNGTSCPSLGGKPKLFFTOACGEGEKDHGFEVAS 300
|||||

OY 301 TSPDESGSNPEPDATPFQGLRTFDQLDAISSLPTSPDIFVSYSYTFPGFVSWRDPKSG 360
|||||
Db 301 TSPDESGSNPEPDATPFQGLRTFDQLDAISSLPTSPDIFVSYSYTFPGFVSWRDPKSG 360
|||||

OY 361 SWYVETLDDIFQWAHSEDLOSLLRVANAVSVKGIYKMPGCCFNFLRKKLFFKTS 416
|||||
Db 361 SWYVETLDDIFQWAHSEDLOSLLRVANAVSVKGIYKMPGCCFNFLRKKLFFKTS 416
|||||

RESULT 2
JC7123
caspase-9 long chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: JC7123
R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A:Reference number: JC7123; MUID:20001956; PMID:10529400
A:Accession: JC7123
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-454 <PU>
A:Cross-references: DDBJ:AB019600; NID:G6440941; PID:G6440942

Query Match 6.7%; Score 28; DB 2 Length 454;
Best Local Similarity 100.0%; Pred. No. 5.5e 20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 CPSLGGKPKLFTIQACGGSEKDHGFEVA 299
|||||
Db 310 CPSLGGKPKLFTIQACGGSEKDHGFEVA 337
|||||

RESULT 3
B88455
protein T15B12.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B88455
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: B88455
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <STO>
A:Cross-references: GB:chr_III; PIDN:AAA21560.1; PID:G540264; GSPDB:GN00021; CESP:T15B12
C:Genetics:
A:Map position: 3

Query Match 2.2%; Score 9; DB 2 Length 370;
```

```
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 IGSGGFGDV 139
|||||
Db 57 IGSGGFGDV 65
|||||

RESULT 4
T09356
brassinosteroid-insensitive protein BR11 - Arabidopsis thaliana
N:Alternate names: protein F23K16.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 24-Nov-1999
C:Accession: T09356
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16652
A:Accession: T09356
A:Molecule type: DNA
A:Residues: 1-1196 <BEV>
A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.30
A:Experimental source: cultivar Columbia; BAC clone F23K16
C:Genetics:
A:Gene: ATSP:F23K16.30; BR11
A:Map position: 4
C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology;

Query Match 2.2%; Score 9; DB 2 Length 1196;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131 IGSGGFGDV 139
|||||
Db 889 IGSGGFGDV 897
|||||

RESULT 5
A69501
hypothetical protein AF2010 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
C:Accession: A69501
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc
; Fleisichmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69501
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-232 <LE>
A:Cross-references: GB:AE000964; GB:AE000782; NID:G2689287; PIDN:AAB89255.1; PID:G26485
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF2010

Query Match 1.9%; Score 8; DB 2 Length 232;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 ESGLRTRT 181
|||||
Db 29 ESGLRTRT 36
|||||

RESULT 6
AE3650
oxidoreductase [EC 1.1.1.-] [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AE3650
```

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A:Reference number: AD3252; PMID:11756688

A:Accession: AE3650

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <KUR>

A:Cross-references: GB:AE008918; PIDN:AAL54368.1; PID:gl7985352; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME11126

A:Map position: 11

C:Keywords: oxidoreductase

Query Match 1.9%; Score 8; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
|||||
DB 103 ALLELARQ 110

RESULT 7

T36004

hypothetical protein SCC22.14c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000

C:Accession: T36004

R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999

A:Reference number: Z21574

A:Accession: T36004

A>Status: preliminary; translated from GB/EMBL/DRBJ

A:Molecule type: DNA

A:Residues: 1-368 <SEE>

A:Cross-references: EMBL:AL096839; PIDN:CAB50757.1; GSPDB:GN00070; SCOEDB:SCC22.14c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCC22.14c

C:Superfamily: Streptomyces coelicolor hypothetical protein SCC22.14c

Query Match 1.9%; Score 8; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EADRRLLR 10
|||||
DB 81 EADRRLLR 88

RESULT 8

G82328

aminotransferase, class V VC0392 [imported] - Vibrio cholerae (strain N16961 serogroup O)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: G82328

R;Heidelberg, J.F.; Eigen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: G82328

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <HEI>

A:Cross-references: GB:AE004127; GB:AE003852; NID:G9654808; PIDN:AAF93565.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor

C:Genetics:

A:Gene: VC0392

A:Map position: 1

C:Superfamily: serine-pyruvate aminotransferase

Query Match 1.9%; Score 8; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCPVSVEK 262
|||||
DB 119 GCPVSVEK 126

RESULT 9

T45344

hypothetical protein MLCB57.28c [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 28-Jul-2000

C:Accession: T45344

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1997

A:Reference number: Z16918

A:Accession: T45344

A>Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-579 <PAR>

A:Cross-references: EMBL:Z99494; PIDN:CAB16668.1

A:Experimental source: cosmid B57

C:Genetics:

A:Note: MLCB57.28c

C:Superfamily: Mycobacterium leprae hypothetical protein MLCB57.28c

Query Match 1.9%; Score 8; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GLRTRTGS 183
|||||
DB 17 GLRTRTGS 24

RESULT 10

T16508

hypothetical protein F59A6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16508

R;Nhan, M. submitted to the EMBL Data Library, December 1995

A:Description: The sequence of *C. elegans* cosmid F59A6.

A:Reference number: Z18526

A:Accession: T16508

A>Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-752 <NHA>

A:Cross-references: EMBL:U41994; NID:gl123051; PID:gl123051; PIDN:AAA83455.1; CESP:F59A

C:Genetics:

A:Gene: CESP:F59A6.4

A:Introns: 43/3; 146/3; 334/1; 400/3; 433/2; 515/3; 672/1

Query Match 1.9%; Score 8; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
|||||
DB 441 GSGGFGDV 448

RESULT 11

T16800

hypothetical protein T05A7.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16800
 R:Chiasoe, S.
 Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of *C. elegans* cosmid T05A7.
 A:Reference number: T18580
 A:Accession: T16800
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-758 <CHL>
 A:Cross-references: EMBL:U40028; NID:G1055143; PID:G1055145; PIDN:AAA81115.1; CESP:T05A7
 C:Genetics:
 A:Gene: CESP:T05A7.6
 A:Introns: 41/3; 142/3; 330/1; 396/3; 439/2; 676/1

Query Match 1.9%; Score 8; DB 2; Length 758;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
 DB 447 GSGGFGDV 454
 |||||

RESULT 12
 T00798
 hypothetical protein At2g32700 [imported] - Arabidopsis thaliana
 A:Alternate names: hypothetical protein F24L7.1
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
 A:Accession: T00798; D84736
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, February 1999
 A:Description: Arabidopsis thaliana chromosome 11 BAC F24L7 genomic sequence.
 A:Reference number: Z14204
 A:Accession: T00798
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-787 <ROU>
 A:Cross-references: EMBL:AC003974; NID:G2914688; PID:G2914703
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, L.;
 eues, D.; Nierman, W.C.; White, O.; Eelen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: D84736
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-787 <STO>
 A:Cross-references: GB:AE002093; NID:G2914703; PIDN:AC04493.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g32700; F24L7.16
 A:Map position: 2
 A:Introns: 11/2; 44/1; 80/3; 174/2; 200/3; 238/1; 254/3; 347/3; 372/3; 446/3; 497/1; 533/1

Query Match 1.9%; Score 8; DB 2; Length 787;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 FGDVGAL 143
 DB 456 FGDVGAL 463
 |||||

RESULT 13
 T23048
 hypothetical protein H05L14.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T23048; T25112
 R:Barlow, K.
 submitted to the EMBL Data Library, October 1997

A:Reference number: Z19662
 A:Accession: T23048
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-794 <WIL>
 A:Cross-references: EMBL:Z99772; PIDN:CAB16921.1; GSPDB:GN00019; CESP:H05L14.1
 A:Experimental source: clone H05L14
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19982
 A:Accession: T25112
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-794 <W12>
 A:Cross-references: EMBL:Z75550; PIDN:CAA99932.1; GSPDB:GN00019; CESP:H05L14.1
 A:Experimental source: clone T22C1
 C:Genetics:
 A:Gene: CESP:H05L14.1
 A:Map position: 1
 A:Introns: 8/1; 61/3; 147/3; 196/3; 231/3; 354/1; 383/2; 437/2; 584/3; 635/3; 658/3; 700/3

Query Match 1.9%; Score 8; DB 2; Length 794;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
 DB 468 GSGGFGDV 475
 |||||

RESULT 14
 E72122
 RNA polymerase beta' - *Chlamydomonas reinhardtii* (strain CWL029)
 C:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 A:Accession: E72122
 R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of *Chlamydomonas reinhardtii* and *C. trachomatis*.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: E72122
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1393 <ARN>
 A:Cross-references: GB:AE001593; GB:AE001363; NID:G4376334; PIDN:AAI8235.1; PID:G43763
 A:Experimental source: strain CWL029
 C:Genetics:
 A:Gene: rPOC
 C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1393;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SEDLQSL 384
 DB 194 SEDLQSL 201
 |||||

RESULT 15
 B86501
 RNA polymerase beta' [imported] - *Chlamydomonas reinhardtii* (strain J138)
 C:Species: *Chlamydomonas reinhardtii*, *Chlamydomonas reinhardtii*
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 A:Accession: B86501
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: B86501
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1393 <STO>

A;Cross-references: GB:BA000008; NID: g8978455; PIDN: BAA98292.1; GSPDB: GN00142
A;Experimental source: strain J138
C;Genetics:

A;Gene: rpoC

C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.7%; Score 8; DB 2; Length 1393;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 SEDLQSL 384
|||||
Db 194 SEDLQSL 201

RESULT 16

E81548

DNA-directed RNA polymerase, beta' chain CP0693 [imported] - Chlamydia pneumoniae (E81548)
C;Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Accession: E81548

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID: 20150255; PMID: 10684935

A;Accession: E81548

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1397 <REA>

A;Cross-references: GB:AE002228; GB:AE002161; NID: g7189606; PIDN: AAF38501.1; PID: g7189606
A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0693

C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1397;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 SEDLQSL 384
|||||
Db 198 SEDLQSL 205

RESULT 17

AE2465

HicA protein [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AE2465

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A;Reference number: AB1807; MUID: 21595285; PMID: 11759840

A;Accession: AE2465

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <KUR>

A;Cross-references: GB:BA000019; PIDN: BAB76976.1; NID: g17134416; GSPDB: GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asl5277

Query Match 1.7%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 TLDDIFE 372
|||||
Db 10 TLDDIFE 16

RESULT 18

T44759

glycine cleavage system protein H [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000

C;Accession: T44759

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, October 1997

A;Reference number: Z22833

A;Accession: T44759

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-132 <PAR>

A;Cross-references: EMBL:AL008609; PIDN: CAA15469.1

A;Experimental source: cosmid B1788

C;Genetics:

A;Gene: gcvH

C;Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology

Query Match 1.7%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 DVGAL 144
|||||
Db 109 DVGAL 115

RESULT 19

B49218

hemagglutinin homolog pmGA1.3 - Mycoplasma gallisepticum (fragment)

C;Species: Mycoplasma gallisepticum

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999

C;Accession: B49218

R;Markham, P.F.; Glew, M.D.; Whithear, K.G.; Walker, I.D.

Infect. Immun. 61, 903-909, 1993

A;Title: Molecular cloning of a member of the gene family that encodes pmGA, a hemagglutinin homolog from Mycoplasma gallisepticum
A;Reference number: A49218; MUID: 93162830; PMID: 8432610

A;Accession: B49218

A;Status: preliminary

A;Molecule type: DNA; protein

A;Residues: 1-135 <MAR>

A;Cross-references: GB:S55216; NID: g265625; PIDN: AAB25398.1; PID: g265627

A;Experimental source: S6

A;Note: sequence extracted from NCBI backbone (NCBIN:125182, NCBIP:125184)

C;Genetics:

A;Genetic code: SGC3

Query Match 1.7%; Score 7; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 TLENLTP 108
|||||
Db 129 TLENLTP 135

RESULT 20

H90776

hypothetical protein ECsll84 [imported] - Escherichia coli (strain O157:H7, substrain R

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C;Accession: H90776

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C. gasawata, N.; Yasunaga, T.; Shibata, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID: 21156231; PMID: 11258796

A;Accession: H90776

A;Status: preliminary

A;Molecule type: DNA

A:Residues: 1-173 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034607.1; PID:gl3360644; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: EC01184

Query Match 1.7%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 PVVLRPE 114
|||||
DB 134 PVVLRPE 140

RESULT 21
DB6609
peptidyl tRNA hydrolase [imported] - Chlamydothila pneumoniae (strain J138)
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: D86609
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: D86609
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-180 <STO>
A:Cross-references: GB:BA000008; NID:g9979324; PIDN:BAA99158.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pth
C:Superfamily: peptidyl-tRNA hydrolase

Query Match 1.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RLVEELO 21
|||||
DB 29 RLVEELO 35

RESULT 22
E72014
peptidyl-tRNA hydrolase CP0909 [imported] - Chlamydothila pneumoniae (strains CML029 and
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: E72014; G81523
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72014
A:Molecule type: DNA
A:Residues: 1-180 <ARN>
A:Cross-references: GB:AE001675; GB:AE001363; NID:g4377273; PIDN:AAD19088.1; PID:g437727
A:Experimental source: strain CML029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
J. C.; Dodson, R.; Quinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: G81523
A:Molecule type: DNA
A:Residues: 1-180 <REA>
A:Cross-references: GB:AE002250; GB:AE002161; NID:g7189821; PIDN:AAF38694.1; PID:g718982
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: pth; CP0909
C:Superfamily: peptidyl-tRNA hydrolase

Query Match 1.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RLVEELO 21
|||||
DB 29 RLVEELO 35

RESULT 23
F71056
hypothetical protein PH148 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: F71056
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71056
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-180 <KAW>
A:Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30248.1; PID:g3257565
A:Experimental source: strain OT3
A:Note: this accession replaces an in-prim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH148

Query Match 1.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELAR 221
|||||
DB 174 ALLELAR 180

RESULT 24
D75088
hypothetical protein PAB0726 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: D75088
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: D75088
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-182 <KAW>
A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50009.1; PID:g54583
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0726

Query Match 1.7%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELAR 221
|||||
DB 176 ALLELAR 182

RESULT 25
G71411
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C:Accession: G71411
 R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terryn, N.; Giel, vanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And C.; Chalwatzis, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
 A:Reference number: A71400; MUID:98121113; PMID:9461215
 A:Accession: G71411
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-182 <BEV>
 A:Cross-references: GB:297337; NID:g2244829; PID:e326833; PID:g2244843
 C:Genetics:
 A:Map position: 4COP9-4G3845

Query Match 1.7%; Score 7; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 NFLRKKL 411
 Db 3 NFLRKKL 9

RESULT 26
 S75396
 hypothetical protein c04030 - Sulfolobus solfataricus
 C:Species: Sulfolobus solfataricus
 C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 17-Mar-1999
 C:Accession: S75396
 R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S. Mol. Microbiol. 22, 175-191, 1996
 A:Title: Organizational characteristics and information content of an archaeal genome: I
 A:Reference number: S73076; MUID:97055432; PMID:8899719
 A:Accession: S75396
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-186 <SEN>
 A:Cross-references: EMBL:Y08257; NID:gl707772; PIR:e281882; PID:gl707802
 A:Experimental source: strain P2
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996

Query Match 1.7%; Score 7; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LFISCLE 78
 Db 42 LFISCLE 48

RESULT 27
 F82448
 conserved hypothetical protein VCA0539 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: F82448
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: F82448
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <HEI>
 A:Cross-references: GB:AE004384; GB:AE003853; NID:g9657936; PIDN:AAF96441.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:

A:Gene: VCA0539
 A:Map position: 2

Query Match 1.7%; Score 7; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 EVKGDLT 208
 Db 121 EVKGDLT 127

RESULT 28
 G82270
 hypothetical protein VC0859 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: G82270
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: G82270
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-200 <HEI>
 A:Cross-references: GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF94021.1; GSPDB:GN00
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0859
 A:Map position: 1

Query Match 1.7%; Score 7; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 EDIQRAG 47
 Db 67 EDIQRAG 73

RESULT 29
 AF2299
 cobalt transport ATP-binding protein cbiO [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AF2299
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguci, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF2299
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA075648.1; PID:gl7133083; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: cbiO
 C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RDQARQL 58
 Db 83 RDQARQL 89

RESULT 30
 E83859
 hypothetical protein BH1677 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: E83859
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hita
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11056132
 A:Accession: E83859
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <STO>
 A:Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA805396.1; GSPDB:GN00
 A:Experimental source: strain C 125
 C:Genetics:
 A:Gene: BH1677
 C:Superfamily: conserved hypothetical protein TM1511
 Query Match 1.7%; Score 7; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 215 ALLELAR 221
 |||||
 Db 207 ALLELAR 213
 |||||
 RESULT 31
 T51025
 hypothetical protein B7F21.60 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
 C:Accession: T51025
 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225286
 A:Accession: T51025
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-234 <SCH>
 A:Cross-references: EMBL:AL389903; GSPDB:GN00116; NCSP:B7F21.60
 A:Experimental source: BAC clone B7F21; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B7F21.60
 A:Map position: 6
 A:Introns: 16/1; 55/2; 70/3; 129/2; 179/3; 196/1
 C:Superfamily: Neurospora crassa hypothetical protein B7F21.60
 Query Match 1.7%; Score 7; DB 2; Length 234;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 94 QAGKLSK 100
 |||||
 Db 137 QAGKLSK 143
 |||||
 RESULT 32
 T13312
 hypothetical protein 23 - Streptococcus phage phi-O1205
 C:Species: Streptococcus phage phi-O1205
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 18-Aug-2000
 C:Accession: T13312
 R:Stanley, E.; Fitzgerald, G.F.; Le Matrec, C.; Fayard, B.; van Sinderen, D.
 Microbiology 143, 3417-3429, 1997
 A:Title: Sequence analysis and characterization of phi O1205, a temperate bacteriophage
 A:Reference number: 217654; MUID:98048466; PMID:9387220
 A:Accession: T13312
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-236 <STA>
 A:Cross-references: EMBL:U08974; NID:g2444080; PID:g2444103; PIDN:AACT9539.1
 A:Experimental source: host Streptococcus thermophilus strain CNR21205
 C:Superfamily: Streptococcus phage phi-O1205 hypothetical protein 23
 Query Match 1.7%; Score 7; DB 2; Length 236;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 LLSRELF 35
 |||||
 Db 177 LLSRELF 183
 |||||
 RESULT 33
 G84678
 Probable RING zinc finger protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84678
 R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.
 eus, D.; Nierman, W.C.; White, O.; Eelen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84678
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-237 <STO>
 A:Cross-references: GB:AE002093; NID:g4510422; PIDN:AA021508.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g27940
 A:Map position: 2
 Query Match 1.7%; Score 7; DB 2; Length 237;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 285 QACGSEQ 291
 |||||
 Db 14 QACGSEQ 20
 |||||
 RESULT 34
 D87435
 transcription regulator, AraC family [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: D87435
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolc
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.N
 proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: D87435
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-240 <STO>
 A:Cross-references: GB:AE005673; NID:g13422878; PIDN:AAK23480.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC1501
 Query Match 1.7%; Score 7; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 136 FGDVGAL 142
 |||||
 Db 73 FGDVGAL 79
 |||||

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RESULT 35
H72691
probable hexulose-6-phosphate synthase APE0952 - Ae. Oryrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H72691
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450, MUID:99110339, PMID:10382966
A:Accession: H72691
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-241 <RAW>
A:Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79936.1; PID:d1041722; PID:9510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0952

Query Match 1.7%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 ALESURG 147
Db 229 ALESURG 235

RESULT 36
C82995
two-component response regulator OmpR PA5200 [imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C82995
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20477337; PMID:10984043
A:Accession: C82995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <STO>
A:Cross-references: GB:AE004933; GB:AE004091; NID:951505; PIDN:AAG0585.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: ompR; PA5200
C:Superfamily: OmpR protein; response regulator homology

Query Match 1.7%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LLSRELF 35
Db 49 LLSRELF 55

RESULT 37
E69455
conserved hypothetical protein AF1646 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: E69455
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

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A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69455
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <LE>
A:Cross-references: GB:AE000989; GB:AE000782; NID:92689312; PIDN:AA889596.1; PID:g26485

Query Match 1.7%; Score 7; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 KPTLENL 106
Db 187 KPTLENL 193

RESULT 38
T18886
hypothetical protein C03D6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18886
R:Burton, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19038
A:Accession: T18886
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-262 <WIL>
A:Cross-references: EMBL:Z75525; PIDN:CAA99766.1; GSPDB:GN00019; CESP:C03D6.1
A:Experimental source: clone C03D6
C:Genetics:
A:Gene: CESP:C03D6.1
A:Map position: 1
A:Introns: 21/2; 58/3; 125/3; 229/2

Query Match 1.7%; Score 7; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 267 FNGTSCP 273
Db 61 FNGTSCP 67

RESULT 39
T06613
hypothetical protein F16J13.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C:Accession: T06613
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoft, A.; Bancroft
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15789
A:Accession: T06613
A:Molecule type: DNA
A:Residues: 1-267 <BEV>
A:Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.130
A:Experimental source: cultivar Columbia; BAC clone F16J13
C:Genetics:
A:Gene: ATSP:F16J13.130
A:Map position: 4
A:Introns: 80/2; 93/2; 130/1; 190/1; 228/2

Query Match 1.7%; Score 7; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 331 A1SSLPT 337
Db 73 A1SSLPT 79

```

```
RESULT 40
JQ0686
nosiheptide resistance protein - Streptomyces actinuosus
C:Species: Streptomyces actinuosus
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Mar-2000
C:Accession: JQ0686
R:Li, Y.; Dosch, D.C.; Strohl, W.R.; Floss, H.G.
Gene 91, 9-17, 1990
A:Title: Nucleotide sequence and transcriptional analysis of the nosiheptide-resistance
A:Reference number: JQ0685; MUID:90382703; PMID:2401410
A:Accession: JQ0686
A:Molecule type: DNA
A:Residues: 1-274 <LIY>
A:Cross-references: GB:U75434; GB:M32744; NID:gl654409; PIDN:AAB17875.1; PID:gl654411
A:Experimental source: ATCC 25421
C:Genetics:
A:Gene: nah
C:Superfamily: conserved hypothetical protein HIC860
C:Keywords: antibiotic resistance

Query Match 1.7% Score 7; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADRRLR 10
Db 156 ADRRLR 162

RESULT 41
T36288
probable ABC-type transport system ATP-binding chain - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T36288
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A:Reference number: 221603
A:Accession: T36288
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <SEE>
A:Cross-references: EMBL:AL049819; PIDN:CAB42665.1; GSPDB:GN00070; SCOEDB:SCE7.06C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE7.06C
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7% Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 LRTRGS 183
Db 243 LRTRGS 249

RESULT 42
E87682
methyltransferase, UbiE/COO5 family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87682
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID: 1259647
A:Accession: E87682
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <STO>
```

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A:Cross-references: GB:AE005673; NID:gl3425221; PIDN:AAK25457.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3495
```

```
Query Match 1.7% Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELAR 221
Db 81 ALLELAR 87
```

```
RESULT 43
B97536
ATP/GTP-binding protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: B97536
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldmar
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97536
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-285 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK87243.1; PID:gl5156529; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_2676
A:Map position: circular chromosome

Query Match 1.7% Score 7; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EADRLR 9
Db 10 EADRLR 16
```

```
RESULT 44
G71276
conserved hypothetical protein TP0829 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: G71276
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: G71276
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <COL>
A:Cross-references: GB:AE001253; GB:AE000520; NID:gl3323131; PIDN:AAC65795.1; PID:gl33231
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0829
```

```
Query Match 1.7% Score 7; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 LLELARQ 222
Db 272 LLELARQ 278
```

RESULT 45

JC1120
 sdsB protein - Pseudomonas sp.
 C:Species: Pseudomonas sp.
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 24-Nov-1999
 C:Accession: JC1120
 R:Davidson, J.; Brunel, F.; Phanopoulos, A.; Prozzi, D.; Terpstra, P.
 Gene 114, 19-24, 1992
 A:Title: Cloning and sequencing of Pseudomonas genes determining sodium dodecyl sulfate
 A:Reference number: JC1118; MUID:92267380; PMID:1587481
 A:Accession: JC1120
 A:Molecule type: DNA
 A:Residues: 1-306 <DNA>
 A:Cross-references: GB:M86744; NID:GL151550; PIDN:AAA25988.1; PID:GL151551
 C:Gene: sdsB
 C:Superfamily: conserved hypothetical protein H11364

Query Match 1.7% Score 7; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELA 220
 |||||
 DB 256 LALLELA 262

RESULT 46
 D75447
 ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: D75447
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: D75447
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-307 <WHI>
 A:Cross-references: GB:AE001953; GB:AE000513; NID:G6458740; PIDN:AAF-0588.1; PID:G645874
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1012
 A:Map position: 1
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7% Score 7; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 VLALLEL 219
 |||||
 DB 125 VLALLEL 131

RESULT 47
 G64456
 conserved hypothetical protein MJ1256 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: G64456
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: G64456
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-311 <BUL>
 A:Cross-references: GB:U67566; GB:L77117; NID:GL1591887; PIDN:AAB99260.1; PID:GL1591890;
 C:Genetics:
 A:Map position: FOR1198613-1199548
 A:Start codon: GTC
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1256

Query Match 1.7% Score 7; DB 1; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 VSVKGIV 397
 |||||
 DB 251 VSVKGIV 257

RESULT 48
 S60713
 polygalacturonase-inhibiting protein - soybean (fragment)
 C:Species: Glycine max (soybean)
 C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 17-Mar-1999
 C:Accession: S60713
 R:Favaron, F.; D'Ovidio, R.; Porceddu, E.; Alghisi, P.
 Planta 195, 80-87, 1994
 A:Title: Purification and molecular characterization of a soybean polygalacturonase-inh
 A:Reference number: S60713; MUID:9515; 48; PMID:7765794
 A:Accession: S60713
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-313 <FAV>
 A:Cross-references: EMBL:X78274; NID:G809547; PID:G809548
 C:Superfamily: polygalacturanase-inhibiting protein; leucine-rich alpha-2-glycoprotein

Query Match 1.7% Score 7; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 PSLGGKP 279
 |||||
 DB 191 PSLGGKP 197

RESULT 49
 AB0350
 probable membrane protein YPO2874 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AB0350
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.F
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0350
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-318 <YUR>
 A:Cross-references: GB:AL590842; PIDN:CAC92125.1; PID:GL15980841; GSPDB:GN00175
 C:Genetics:
 A:Gene: YPO2874

Query Match 1.7% Score 7; DB 2; Length 318;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLRRCL 14
 |||||
 DB 25 LLRRCL 31

RESULT 50

A72637
 hypothetical protein APE1552 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-199 #text_change 20-Aug-1999
 C:Accession: A72637
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Min-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: A72637
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-319 <RAW>
 A:Cross-references: DDBJ:AP000061; NID:q5104821; PIDN:RAA805511; PID:d1044337; PID:q510
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1552

Query Match 1.71; Score 7; DB 2; Length 319;
 Best Local Similarity :00.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	46	AGSGSRR	52
DB	306	AGSGSRR	312

Search completed: October 20, 2003, 12:27:58
 Job time : 48 secs